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1: pir1:*
2: pir2:*
3: pir3:*
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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plasma kallikrein
plasmin (EC 3.4.21
complement factor
plasmin (EC 3.4.21
coagulation factor
hepsin (EC 3.4.21
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membrane-bound arginine-specific serine proteinase precursor - x C;Species: Rattus norvegicus (Norway rat)
C;Ante: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change | C;Accession: JC7731, JC7775
R;Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.;
J. Biochem. 130, 425-430, 2001
A;Title: Characterization of a membrane-bound arginine-specific | A;Accession: JC7731
A;Accession: JC7731
A;Accession: JC7731
A;Accession: JC7731
A;Molecule type: mRNA
A, Polecule type:
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A;Experimental source: strain Male, 7-week-old
R;Satomi, S.; Yamasaki, Y.; Tsuxuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001
A;Title: A role for membrane-type serine protease (MT-SP1) in intestinal epithelial A;Reference number: JC7775; PMID:11573963
A;Contents: Small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: basolateral cell surface C;Superfamily: membrane-bound arginine-specific serine proteinase C;Keywords: protein digestion
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C;Comment: This enzyme, an epithelial-derived, type II integral membrane of specific proteins or peptides on the brushborder membranes. It also plial migration and/or cell loss.
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A; Residues: 1-855 <SAT>
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80.8%; Pred. No. 6.1e-245;
tive 79; Mismatches 85;
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N;Alternate names: enterokinase
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
C;Accession: A53663
C;Accession: A536663
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A; Accession: A53663
                                                                                                                                                                                                                                                                                                                                                                                enteropeptidase (EC 3.4.21.9) precursor [validated]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 DRGFRYSDFTOWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDETFDYDIALLELEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLIS$NWLVSAAHCYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIPEVROWIKEQTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEYSTVVRPICLPDNTHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTCEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETIFKYSDHTMWTAFLGLLDQSKRSASGVQEHKLKRIITHPSFNDFTFDYDIALLELEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCDCGLRSFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855
                                                                                                                                                                                                                                                                                                                                                                                         pig
                                                                                                                                                                             Miki, K.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840
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                                                                                                                                                                             Kurokawa,
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A;Description: cleaves activation peptide from trypsinogen to produce active trypsin A;Description: cleaves activation peptide from trypsinogen to produce active trypsin A;Pathway: intestinal digestive hydrolase cascade

C;Superfamily: enteropeptidase; Cir/Cls repeat homology; LDL receptor ligand-binding repe

C;Reywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen

F;22-38/Domain: transmembrane #status predicted <MCH>
F;22-13/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-799/Product: enteropeptidase heavy chain #status predicted <MCH>
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;357-519/Domain: MAM homology <MAM>
F;351-646/Domain: MAM homology <MAM>
F;351-649/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRCF
F;800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F;800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F;907-911,925-941,925-992,956-971,992-1010/Disulfide bonds: #status predicted
F;787-911,825-841,925-992,956-971,982-1010/Disulfide bonds: #status predicted
F;7840,891,986/Active site: His, Asp, Ser #status predicted A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1034 cMAT>
A; Residues: 1-1034 cMAT>
A; Cross-references: GB:D30799; NID:g505122; PIDN:BAA06459.1; PID:g505123
A; Note: parts of this sequence, including the amino ends of three chains isolated
C; Comment: The mechanism of association with the membrane of the intestinal brush
otated below) or with amino-terminal myristroylation of the heavy chain.
C; Complex: Mature enteropeptidase is variously reported to contain two (heavy and C; Function: Similarity 15.5%; Score 724; DB 1 Pred. No. 2e-39; 5; Mismatches 3 DB 1; light) involve from the

Ş

Conservative

55 WVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQK--VKNGYMRIT-----NENFVDAYEN 107 : | |:|: | | | |

330;

Indels

360;

Gaps

compo

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-PGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVN 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPFVKLNTAP------NGSLILTASEQC--FEDSLILLQCNHKS------CGKKQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEVSPKIVGGNDSREGAWPWVVALYYNGQ-LLCGASLVSRDWLVSAAHCVYG----RNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQA--RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KVNVVTCTKHTYRCLNGLCLSKGNPECDGKED-----CSDGSDEKDCDCGLRSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTANNSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEDNFQCENGECVLLVNLCDGFSHCKDGSDEAHCV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGEK----YCGERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLS---YDSSDPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LTFHSSQNVLLITLITNTERRHPGF-----EATFF-----QLPRMSSCGG--RLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLWLMNPGTIRIFSNQVTVTFLIESDENDYIGFNATYTAFNSTELNNDEKINCNFEDGFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIECLPGSRPCADALKCIAVDLFCDGELNCPDGSDEDSKICATACD-----
WIQ 1030
                                                                      WIK 850
                                                                                                                                                      MMCAGYEEGGIDSCQGDSGGPLMCLE-NNRWLLAGVTSFGYQCALPNRPGVYARVPKFTE
                                                                                                                                                                                                                                 MMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRD 847
                                                                                                                                                                                                                                                                                                                PICLPEENQVFPPGRICSIAGWGKVIYQGSPADILQEADVPLLSNEKCQQQMPEYNITEN
                                                                                                                                                                                                                                                                                                                                                                                           PICTPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQ-QITPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSKWKAILGLHMTSNLTSPQIVTRLIDEIVINPHYNRRKDSDIAMMHLEFKVNYTDYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCGDNSDEQGCSCPAQTFRCS---NGKCLSKSQQCNGKDDC---GDGSDEASCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGEEDDSLLLAVYTGPGPVEDVFSTTNRMTVLFITNDALTKGGFKANFTTGYHLGIPEPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPNTTFTSMNFPNNYPNQAFCVWNLNAQKGKNIQLHFEEFDLENIA------DVVBIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEI- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFKVAFNAFKNQFLSDIALDDISLTYGICNVSLYPEPTLVPTSPPELP--TDCGGPFELW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-TLEPVCLSFWYYMYGENVYKLSINISNDQNMEKIIFQKEGNYGENWNYGQVTLNETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FWIQDLNDDNEWERIQGTTFPPFTGPNFDHTFGNASGFYISTPTGPGGRQERVGLLSLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSFDAAQYPKLSEASVVCQWIIRVNQGLSIELNFSYFNTYSMDVLNIYEGVGSSKILRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LP---PRARSLKSFVV----TSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKEELIQGIEANKSSQLVAFHIDVNSIDITESLENYSTTSPSTTSDKLTTSSPPATPGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I PQHLVEEAERVMAEERVVM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTALFAILMVLCAGLIAVSWLTIKGSEKDAALGKSHEARGTMKITSGVTYNPNLQDKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SVDFKVLAFDIQQMIGEIFQSSNLKNEY-KNSRVLQFENGSVIVIFDLLFAQWVSDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LVQFRIQSIWHTACAENWTTQTSDDVCQLLGLGTGNSSMPFFSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RF-----LN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: cleaves propeptide from trypsinogen to produce active trypsin A;Pathway: intestinal digestive hydrolase cascade C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat product: enteropeptidase; intestine; serine proteinase; transmembrane protein, F;22-38/Domain: transmembrane #status predicted <NPM>
F;22-38/Domain: transmembrane #status predicted <NPM>
F;52-117/Product: enteropeptidase mini chain #status predicted <HCH>
F;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;358-520/Domain: MAM homology <MAM>
F;452-647/Domain: C1r/C1s repeat homology <C1R>
F;654-693/Domain: LDL receptor ligand-binding repeat homology #status atypical <SRCF F;694-799/Domain: Bcavenger receptor cysteine-rich domain homology #status atypical <SRCF F;801-1036/Product: enteropeptidase light chain #status predicted <LCH>
F;116,147,170,194,233,263,264,404,455,486,519,550,646,698,722,741,762,864,903,965/Binding F;881,892,987/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: parts of this sequence, including the amino end of the mature protein, were configit, A.; Janaka, H.
J. Protein Chem. 10, 475-480, 1991
A,Fritle: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
A,Reference number: A61436; MUID:92189715; PMID:1799406
A,Rolecule type: protein
A;Residues: 801-807,'Y',809-827 <LIG>C;Comment: The mechanism of association with the membrane of the intestinal brush border embrane attachment using a signal-anchor sequence.
C;Comment: Conversion from membrane-bound to soluble forms may involve further processing C;Complex: mature enteropeptidase is variously reported to contain two (heavy and light)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Residues: 801-1035 < LAV>
A; Cross-references: GB:L19663; NID:g416131; PIDN:AAA16035.1; PID:g416132
A; Cross-references: GB:L19663; NID:g416131; PIDN:AAA16035.1; PID:g416132
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A;Residues: 1-1035 KITS
A;Rersidues: 1-1035 KITS
A;Rersidues: 1-1035 KITS
A;Rersidues: 1-1035 KITS
A;Cross-references: UNIPROT:P98072; GB:U09859; NID:g746410; PIDN:AAB40026.1; PID:g746411
A;Experimental source: small intestine
R;LaVallie, E.R.; Rehemtulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.; I
J. Biol. Chem. 268, 23311-23317, 1993
A;Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of bc
A;Reference number: A48874; MUID:94043122; PMID:8226855
A;Accession: A48874
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A43090; A48874; Ā61436
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic p: A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic p: A;Reference number: A43090; MUID:94329561; PMID:8052624
A;Reference number: A43090
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
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                                     165
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                             LVEEAERVMAEERVVM---
                                                                                                                DFKVLAFDIQQMIDDIFQSSNLKNEY-KNSRVLQFENGSIIVIFDLLFDQWVSDKNVKEE 139
                                                                                                                                                                                                                                                                              FAVLFVILVALCAGLIAVSWLSIQGSVKDAAFGKSHBARGTLKIISGATYNPHLQDKLSV
                                                                                                                                                                                                                                                                                                                                                         WVVLAAVLIGLLLVLLGIGFLVWHLQYRDV---RVQKVKNGYMRITNENFVDAYENSNST
                                                                                                                                                                                           EFVSLASKVKDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYY-----W-SEFSIPQH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                15.2%; Score 709.5;
23.1%; Pred. No. 1.70
tive 150; Mismatches
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                                 -LPPRARSLKSFVVTSV-----V 197
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enteropeptidase (EC 3.4.21.9) precursor N;Alternate names: enterokinase C;Species: Homo sapiens (man) C;Date: 19-May-1995 #sequence revision 0
                                                                         RESULT
A56318
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                                                                                                                                                                                  FRDWIK 850
                                                                                                                                                                                                                     TENMVCAGYEAGGVDSCQGDSGGPLMCQE-NNRWLLAGVTSFGYQCALPNRPGVYARVPR
                                                                                                                                                                                                                                                     TPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPL 844
                                                                                                                                                                                                                                                                                          YIQPICLPEENQVPPPGRICSIAGWGALIYQGSTADVLQEADVPLLSNEKCQQQMPEYNI
                                                                                                                                                                                                                                                                                                                           MVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQ-QI
                                                                                                                                                                                                                                                                                                                                                              NMEPSKWKAVLGLHMASNLTSPQIETRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTD
                                                                                                                                                                                                                                                                                                                                                                                               YSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFTRQA--RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPTFSTGGGPYVNLNTAP-----NGSLILTPSQQC-----LEDSLILLQCNYKSCGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLGIPEPCKEDNFQCKDGECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -YDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSDELNC----SCDAGH--QFTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNETVEFKVSFYGFKNQILSDIALDDISLTYGICNVSVYPEPTLVPTPPPELP--TDCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFCFWIQDLNDDNEWERTQGSTFPPSTGPTFDHTFGNBSGFYISTPTGPGGRRERVGLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDS-----PYPAH---ARCOWALRGDADSVLSLTFRSFD
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                                                                                                                                                 FTEWIQ 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIQGIEANKSSQLVTFHIDLNSIDITASLENFSTISPATTSEK--LTTSIPLATPGNVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASLWSNNPG1IRIFSNQVTATFLIQSDE--SDYIGFKVTYTAFNSKELNNYEKINCNFED
   #sequence_revision 09-Aug-1996
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                                                          [validated]
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     09-Jul-2004
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A; Description: cleaves activation peptide from trypsinogen to produce active trypsin A; Pathway: intestinal digestive hydrolase cascade
C; Superfamily: enteropeptidase; Clr/Cls repeat homology; LDL receptor ligand-binding
C; Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymog
F;1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
F;22-38/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;342-504/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;342-504/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;643-677/Domain: Clr/Cls repeat homology <Clr>
F;643-677/Domain: Scavenger receptor cysteine-rich domain homology #status atypical
F;785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F;785-1014/Domain: trypsin homology <TRY>
F;116,147,179,318,335,388,440,470,503,534,630,682,706,725,848,887,909,949/Binding si
F;772-886,810-826,910-977,441-956,967-995/Disulfide bonds: #status predicted
F;825,876,971/Active site: His, Asp, Ser #status predicted
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A;Residues: 1-10.9 kTT>
A;Cross-references: UNIPROT:p98073; GB:U09860; NID:g746412; PIDN:AAC50138.1;
A;Cross-references: UNIPROT:p98073; GB:U09860; NID:g746412; PIDN:AAC50138.1;
A;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic prof;Reference number: A43090, MUID:94329561; PMID:8052624
A;Accession: B43090
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A;Map position: 21q21-21q21
C;Complex: Mature enteropeptidase is various
ed by a disulfide bond. Possibly, conversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 749-1019 <KI2>
A;Cross-references: GB:U09860
C;Comment: The mechanism of association with the membrane of the otated below) or with amino-terminal myristoylation of the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A56318; B43090
R;Kitlamoto, Y.; Veile, R.A.; Donis-Keller, H.; Sadler, J.E. Biochemistry 34, 4562-4568, 1995
A;Title: CINA sequence and chromosomal localization of human A;Reference number: A56318; MUID:95234679; PMID:7718557
A;Accession: A56318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 GVPAGTCPKDYVEI-NGEK-----YCGERSQFVVTSNSNKITVRFHSDQSYTDTGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP
HKSCGKKLAAQDITPKIVGGSNAKEGAWPWVVGLY-YGGRLLCGASLVSSDWLVSAAHCV
                                                            EKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCY
                                                                                                                                                                                                     GDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDG-----KEDCSDGS-----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELP--TDCGGPFELWEPNTTFSSTNFPNSYPNLAFCVWILNAQKGKNIQLHFQEFDLEN-
                                                                                                                                                                                                                                                                            TTNNNGLVRFRIQSIW----HTACAEN--
                                                                                                                                                                                                                                                                                                                                         TCKN----KFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEYLS --- YDSSDPCPG-QFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQF---
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Pred. No. 1.0
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A;Molecule type: mRNA
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A;Residues: 1-1113 <TOM>
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A;Residues: 1-1113 <TOM>
A;Residues: 1-1113 <TOM>
A;Cross-references: UNIPROT:Q9Z319; DDBJ:AB013874; NID:g3869144; PIDN:BAA34371.1; PID:g3
C;Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor ligand-binding repeat homology <LDL1>
F;337-372/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;440-448/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;648-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;648-720/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;669-1097/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;869-1097/Domain: LDL receptor ligand-binding repeat homology <LDL7>
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                                                                                                                                                                                    R-QARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDP
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                                     ICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQ-ITPRM 788
                                                                                                            TQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRP 729
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ilarity 32.7%;
Conservative 6
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C;Accession: T30337

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C;Superfamily: tryosin related polyprotein; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyprotein - African clawed frog C;Species: Xenomie lacti- /-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDB
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;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: tryosin related polyprotein; trypsin homology;
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QPALGLQQLQLPILDSIICNTSYYSGELTDHMLCAGFPSSKEKDACQGDSGGPLVCQNEK 778
                                                                                                                    RIHDNYNSETYDNDIALLYLEEPLDLNDFYRPYCLPEPEEVLTPASVCVVTGWGNTAEDG
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                                                        TGALILOKGEIRVINOTTCE-NLLPQQITPRMMCVGFLSG-GVDSCQGDSGGPLSSVEAD
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A, Map position: 3q27-3q28

C:Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat homology complement activating serine proteases Clr/Cls/MASP; Clr/Cls repeat homology cisconding special sequence #status predicted cs[Gs]

F:18-148,449-699/Broduct: Ra-reactive factor #status predicted cMAT>
F:19-135/Domain: signal sequence #status predicted cs[Gs]
F:18-294/Domain: Clr/Cls repeat homology cClRl>
F:18-294/Domain: Clr/Cls repeat homology cClR2>
F:185-294/Domain: Clr/Cls repeat homology cClR2>
F:367-432/Domain: complement factor H repeat homology cFH1>
F:367-432/Domain: complement factor H repeat homology cFH2>
F:449-691/Domain: trypsin homology cTRY>
F:449-691/Domain: trypsin homology cTRY>
F:491.178.407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:39-71.143-157.153-166,168-181.185-212,242-260.301-349,329-362,367-414,397-432,436-572
F:159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
F:490,552,646/Active site: His, Asp, Ser #status predicted
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A;Title: A new member of the CIs family of complement proteins A;Reference number: JN0883; MUID:94059062; PMID:8240317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-234;E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699
A;Crose-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
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A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JN0883
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names: mannose binding protein-associated serine proteinase 1 (MASP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                      SSQNVLLITLITUTERRHPGFEATFFQLP-----
                                                                                                                                                                                                                                                                                                                                                                                                FDLASCDERGSDLVTVYNTLSPMEPHALVQLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS
                                                       FYLLE--PGVPAGTCPKDYVEIN-GEK----YCGERSQFVVTSNSNKITVRFHSDQSYTD 437
                                                                                                                                                                                                                               SD-----FSNEERFTGFDAHYMAVDVDECKEREDEELSCDHYCHNYIGGYYCSCRF
                                                                                                                                                                                                                                                                                                                                           FNLESSYLCEYDYVKV----ETEDQVLATFCGRETTDTEQTPGQEVVLSPGSFMSITFR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKASAHTVELNNMFG-----QIQSPGYPDS-YPSDSEVTWNITVPDGFRIKLYFMH
                                                                                                               GYILHTDNRTCRVECSDNLFTQRTGVITSPDFPNPYPKSSECLYTIELEEGFMVNLQFED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                    RMSSCGGRIRKAOGTFNSPYYPGHYPPNIDCTWNIEVPNNOHVKVRFKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.2%; Score 570; DB 1; Length 699; 25.3%; Pred. No. 1.5e-29; tive 111; Mismatches 268; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:BAA05928.1; PID:g47112
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A;Note: part of this sequence, including the amino ends of both the heavy and light chair
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex wi
C;Comment: The zynogen is activated by factor XIIa, which cleaves the molecule into a lig
are linked by one or more disulfide bonds.
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflan
F;1-19/Domain: signal sequence #status predicted <SIG-
F;20-199/Domain: signal sequence #status predicted <SIG-
F;20-199/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;301-289/Domain: apple repeat <AP2>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;27,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-
F;21-194,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-
F;313-34,483,578/Active site: His, Asp, Ser #status predicted
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A;Molecule type: mRNA
A;Residues: 1-638 <SEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, DNA Cell Biol. 9, 737-748, 1990
A;Tille: Mouse plasma kallikrein: cDNA structure, enzyme chara;Reference number: A36557; MUID:91090844; PMID:2264928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasma kallikrein (EC 3.4.21.34) precursor - C;Species: Mus musculus (house mouse) C;Date: 30-Sep-192 #sequence_revision 30-Sep C;Accession: A36557
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KQMSPL
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                                                       271 RGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGF--E
                                                                                                                                            Similarity
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                                                                                                               Conservative
                                                                                                                                         11.3%;
27.2%;
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                                                                                                                                         Score 528.5;
Pred. No. 6.8
                                                                                                               Mismatches
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                                                                                                               175;
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comparisor Rochemon

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RESULT 9

KORTPL

Plasma kallikrein (EC 3.4.21.34) precursor - rat

N.Alternate names: Fletcher factor; kininogenin; serum kallikrein

C;Species: Rattus norvegicus (Norway rat)

C;Actes (C) - Sep. 1992 #sequence revision 30.5ep-1992 #text_change 09-Jul-2004

C;Acces (C) - Sep. 1992 #sequence ration (S) - Sep. 1991

R;Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.

Biochemistry 30, 1628-1635, 1991

A;Title: Gene structure and chromosomal localization of plasma kallikrein.

A:Poference number: A39180; MUID:91129236; PMID:1993180
            A;Cross-references: GB:M30282; NID:g205010; PIDN:AAA41463.1; PID:g205011 A;Note: part of this sequence, including the amino ends of both the heavy R;Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, Biochim. Biophys. Acta 999, 103-110, 1989
                                                                                                                                                                                                      A;Cross-references: UNIPROT:P14272; GB:J05315
A;Note: the authors translated the codon GAG for rei
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin,
DNA 8, 563-574, 1989
                                                                                      A; Molecule type: mRNA
A; Residues: 1-638 <SEI>
                                                                                                                                              A;Title: The cDNA structure A;Reference number: A33320; A;Accession: A33320
                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-638 < BEA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPKD-----YVEINGEKYCGERS---QFVVTSNSNKITVRFHSDQSYTDTG----FLAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCGLRSFTRQARVVGGTDADEGEWPWQVSLHA---LGQGHICGASLISPNWLVSAAHCYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DGSP----TRITYGMQGSSGYSLRLCKLVDSPDCTTKIN-----
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                                                                                                                                                                  of rat plasma kallikrein.
MUID:90091743; PMID:2598771
                                                                                                                            conceptual translation
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A; Gene: PK
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C; Keywords:
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Best Local
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                SIIGRQWILTAAHCF---DGIPY--PDVWRIYGGILNLSEITNKTP---FSSIKELIIHQ
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C.Superfamily: coagulation factor XI; trypsin homology
C.Superfamily: coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflan
C.Keywords: blood coagulation; duplication; fibrinolysis;
F.1-19/Domain: signal sequence #status predicted <SIG>
F.20-390/Product: plasma kallikrein heavy chain #status experimental <MATI>
F.20-109/Domain: apple repeat <APP>
F.100-199/Domain: apple repeat <APP>
F.201-289/Domain: apple repeat <APP>
F.201-380/Domain: apple repeat <APP>
F.201-380/Domain: apple repeat <APP>
F.201-380/Domain: apple repeat <APP>
F.301-380/Product: plasma kallikrein light chain #status experimental <MAT2>
F.301-631/Product: plasma kallikrein light chain #status experimental <MAT2>
F.301-301/Product: plasma kallikrein light chain #status experimental <MAT2>
F.301-301/Product: plasma kallikrein light chain #status experimental <MAT2>
F.301-301/Product: plasma kallikrein light chain #status experimental <MAT2>
F.301-301/Productive site: His, Asp, Ser #status predicted
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A;Residues: 20-45;391-413 <PAQ>
R;Seidah, N.G.; Ladenhein, R.; Mbikay, M.;
DNA Cell Biol. 8, 563-574, 1989
A;Title: The cDNA structure of rat plasma k
A;Reference number: I53041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Rat plasma kallikrein: purification, NH(2)-terminal sequencing A;Reference number: S06851; MUID:90089457; PMID:2597701 A;Accession: S06851.
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SLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQ--RSAPGVQERRLKRIISHP
                                                                                                SSGYSLRLCKVVESSDCTTKI-----NARIVGGTNSSLGEWPWQVSLQVKLVSQNHMCGG
                                                                                                                                                                                                                                                                                                                                                            D--EASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCS----DGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSKSGRPSPPIIQENAVSGYSLFTCRK---
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                                                                                                                                                                                                                                                                     DACQETCTK--TIRCQFFTYSLLPQDCKAEG---C---KCSLRLSTDGSPTRITYEAQG
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Pred. No. 1.6e-1
79; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ARPEPCHFKIYSGVAFEGEELNATFVQGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -WVCDSV-NDCGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209;
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A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a value of the graafian follicle; also activates the urokinase-type plasminogen act A;Pathway; fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasmin; protein precursor homology fileroduct: plasminogen #status predicted <PRO>
F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F;1-77/Domain: plasmin chain A #status predicted <APT>
F;1-77/Domain: activation peptide #status predicted <APT>
F;1-77/Domain: kringle homology <KR1>
F;4-1-62/Domain: kringle homology <KR2>
F;3-58-435/Domain: kringle homology <KR2>
F;3-6-333/Domain: kringle homology <KR2>
F;3-58-435/Domain: kringle homology <KR3>
F;3-58-435/Domain: kringle homology <KR4>
F;4-50-790/Product: miniplasminogen #status experimental <MIN>
F;4-1-790/Product: miniplasminogen #status experimental <BCH>
F;5-1-793/Domain: kringle homology <KR4>
F;3-1-793/Domain: kringle homology <KR4-
F;3-1-793/Domain: kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: protein
A; Residues: 1-57 <BRU's
R, Marti, T.; Schaller, J.; Rickli, E.E.
RLUR. J. Biochem. 149, 279-285, 1985
Eur. J. Biochem. 149, 279-285, 1985
A, Fittle: Determination of the complete amino-acid sequence
A; Fittle: Determination of the complete amino-acid sequence
A; Reference number: A25834; MUID:85203907; PMID:3846533
A; Accession: A25834
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 450-790 <MAR>
C; Function:
C; Pescription: dissolves the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P06867
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Le Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal A;Reference number: S03735; MUID:B1212097; PMID:7238497
A;Accession: S03737
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PLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change
C;Accession: S03733; S03737; A25834
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A; Molecule type: protein
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SPIARMRDVVLFEKRIYLSECKTGNGKNYRGTTSKTKSGVICQKWSVSSPH
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Pred. No. 2.4e
00; Mismatches
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                           GVVSWGDGCAGRNKPGVYTRLPLFRDWIKE
                                                                                                                                                                                                 NDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALIL
                                                                                                                                                                                                                                                                                                                                                                NPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EINGBKYCGERSOFVVTSNSNK-ITVRFHSDQ----SYTDTGFLAEYLSYDSSDPCPGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPKYSPEKFPLAGLEENYCRNPDNDEK-----GPWCYTTDPET--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPQHLVEEAERVMAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHA
GVTSWGLGCALPNKPGVYVRVSRFVTWIEE
                                                                            KEARLPVIENKVCNRYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVCFEKDKYIL-Q
                                                                                                                  QXGEIRVINQTTCE--NLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGA
                                                                                                                                                             ----SEADIALLKISSPAVITOKVIPACLPTPNYVVADRTACYITGWGETK-GTYGAGLL
                                                                                                                                                                                                                                         TLISPEWVLTAKHCL----EKSSSPSSYKVILGAHEE-YHLGEGVQEIDVSKLFKEP--
                                                                                                                                                                                                                                                                                                                                                                                                          NPQKLFDYCDVPQCVTSS----FDCGK-----PKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                        -PAQTF-RCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEENYCRNPDGETAPWCYTTDSEVRWDYCKIPSCGSSTTSTEHLDAPVPPEQTPVAQDCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEV-----PNNOHV------KVRFKFFYL------LEPGVPAGTCP--KDYV
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                                                                                                                                                                                                                                                                                                                            -EPKKC-----PARVVGGCVSIPHSWPWQISLRYRYRGHFCGG
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785
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complement C3b/C4b inactivator (EC 3.4.21.-) precursor - African N,Alternate names: C3b/C4b inactivator factor I C;Species: Xenopus laevis (African clawed frog) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change C;Accession: I51601; S15468 G.H.; Sim, R.B.; Day, A.J.; Ezeko R;Kunnath-Muglia, L.M.; Chang, G.H.; Sim, R.B.; Day, A.J.; Ezeko Mol. Immunol. 30, 1249-1256, 1993 A;Title: Characterization of Xenopus laevis complement factor I A;Reference number: I51601; MUID:94019415; PMID:7692240 A; Reference number: A; Accession: I51601 A; Molecule type: A; Status: preliminary; translated mRNA from GB/EMBL/DDBJ African Ezekowitz, structure--conservation 09-Jul-2004 clawed R.A.

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A;Gene: Sb-sbd
A;Cross-references: FlyBase:FBgn0003319
C;Superfamily: serine proteinease stubble-stubbloid; trypsin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;61-77/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                   R;Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds, A.; G
Proc. Natl. Acad. Sci. U.S.A. 90, 4937-4941, 1993
A;Title: The Drosophila Stubble-stubbloid gene encodes an
A;Reference number: A47547; MUID:93281671; PMID:7685111
A;Accession: A47547
A;Status: preliminary
                                                                                                                                                                                                                                                                                               RESULT 12
A47547
serine proteinease stubble-stubbloid (EC 3.4.21.-) - fruit fly (C;Species: Drosophila melanogaster
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:003711; EMBL:X59958; NID:g64595; PIDN:CAA42582.1; PID:g64596 C;Superfamily: human complement factor I; LDL receptor ligand-binding repeat homology; t C;Keywords: hydrolase; serine proteinase r;220-254/Domain: LDL receptor ligand-binding repeat homology <LDL1> F;257-290/Domain: LDL receptor ligand-binding repeat homology <LDL1> F;257-290/Domain: LDL receptor ligand-binding repeat homology <LDL2>
                                                                                                              A;Molecule type: mRNA
A;Residues: 1-786 <APP>
A;Cross_references: UNIPROT:Q05319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEPGKGIIKVKLPTFEQELFLCGKQWSNREANVVCRQLGSTKGADASASDKVFSLVTEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPKNATTEVCTDGKRKLQSYCQLKS--VECSNPLNSKYRFSSEAPCTETFTLTQ-----N 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPKD---YVEINGEK----YCGERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R-EKGMSRVFHLKWGHINLMD--NCTRVYKERFLDKMECARTYDGSIDACKGDSGGPLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIYIGGCWVLTAAHC-----VRSNQPQRYLIMLELLDRLSYDKDLDSFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACDSKNDCGDLSDELCCKSCNA-GFHCRSDTCIPEQYRCNGELDCIGGEDESNCTVEQEQ
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Pred. No. 2.
                                                                                                                  GB:L11451;
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                                                                                                              NID:g158511;
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                                                                                                                                                                                                                                                                                         DCGLRSFTR-QARVVGGTDADEGEWPWQVSLH----ALGQGHICGASLISPNWLVSAAH
CAEANLPGVCTRISKFTPWILEH
                                                              NCKSMFMRAGRQEFIPDIFLCAGYETGGQDSCQGDSGGPLQAKSQDGRFFLAGIISWGIG
                                                                                                                           VKLEQPLEFAPHVSPICLPETDSLL-IGMNATVTGWGRLSEGGTLPSVLQEVSVPIVSND
                                                                                                                                                           LELEKPABYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQT
                                                                                                                                                                                                                         CYIDDRGFRYSDPTQWTAFLGLHDQS--QRSAPGVQERRLKRIISHPFFNDFTFDYDIAL
                                                                                                                                                                                                                                                         ECGVPTLARPETRIVGGKSAAFGRWPWOVSVRRTSFFGFSSTHRCGGALINENWIATAGH
                              CAGRNKPGVYTRLPLFRDWIKEN 852
                                                                                           TCENLL----PQQITPRM-MCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDG
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                                                                                                                                                                                                                                                                                                                                       10.6%;
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                                                                                                                                                                                                                                                                                                                                        Score 495.5; DB 1
Pred. No. 1.2e-24;
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plasma kallikrein (EC 3.4.21.34) precur
N;Alternate names: kininogenin; plasma
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence revision
C;Accession: A00921; A37939
R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W. Biochemistry 25, 2410-2417, 1986 Biochemistry 25, 2410-2417, 1986 A;Title: Human plasma prekällikrein, a zymogen to a serine A;Reference number: A00921; MUID:86243359; PMID:3521732
                                                                                                                                                                                                               (EC 3.4.21.34) precursor - human kininogenin; plasma prekallikrein
                                                                                                                                                      13-Aug-1986
                                                                                                                                                          #text_change
                                     protease
                                                                                                                                                                09-Jul-2004
                                        that
                                        contains
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four

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A;Cross-references: UNIPROT:P03952; GB:M13143; NID:g19020; R;McMullen, B.A.; Fujikawa, K.; Davie, E.W. Biochemistry 30, 2050-2056, 1991
A;Title: Location of the disulfide bonds in human plasma A;Reference number: A37939; MUID:91152016; PMID:1998666
A;Accession: A37939 A;Residues: 1-638 <CHU> NID:g190262; PIDN:AAA60153 PID:g190263 of f

prekallikrein:

the

A; Molecule type: mRNA A; Accession: A00921

A;Molecule type: protein
A;Residues: 20-27;40-46, 'X', 48, 'H';50, 'X',52-70, 'H';75-76, 'X',78-80;103-113;131-140;141-:
A;Residues: 20-27;40-46, 'X',293-295;314-317, 'X',319-320;321-324;'X',329-333;334-339,'X',
260-283,'X',285;287-291,'X',293-295;314-317,'X',319-320;321-324;'X',329-333;334-339,'X',
525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 «MCM»
C;Comment: The protein, synthesized in the liver, circulates as a noncovalent complex w:
C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a liq
are linked by one or more disulfide bonds.
C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal ratiogen and may also play a role in the renin-angiotensin system by converting prorenin in C;Genetics:
A;Gene: GDB:KLK3
A;Cross-references: GDB:127575; OMIM:229000
A;Map position: 4q35-4q35
C;Superfamily: coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflam F;1-19/Domain: signal sequence #status predicted <81G-XMT.

Superfamily: coagulation factor XI; trypsin homology; Keywords: blood coagulation; duplication; fibrinolysis; gl; Keywords: blood coagulation; duplication; fibrinolysis; gl; 1-19/Domain: signal sequence #status predicted <MAT>; 20-638/product: plasma kallikrein #status predicted <MAT>; 20-390/Domain: plasma kallikrein heavy chain #status predicted; 20-109/Domain: apple repeat <AP1>

predicted

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plasmin (BC 3.4.21.7) precursor - sheep (
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Ovis orientalis aries, Ovis am
C;Date: 28-Oct-1994 #sequence revision Ol
C;Accession: B61545; S28200
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasmi
A;Reference number: A61545; MUID:89005015
A;Accession: B61545
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B61545
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F;390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status
F;434,483,578/Active site: His, Asp, Ser #status predicted
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;Molecule type: protein
;Residues: 1-37;38-117 <SCH>
;Cross-references: UNIPROT:P81286
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Similarity 26.8%; Pred. No. 1e-24;
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                                                              of the plasminogen of various MUID:89005015; PMID:3168975
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#text_change 09-Jul-2004
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R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 5, 21-25, 1992

A;Title: Complete amino acid sequence of ovine miniplasminogen.

A;Reference number: S28200; MUID:9314995; PMID:1492092

A;Recession: S28200

A;Molecule type: protein

A;Residues: 118-460 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology; C;Superfamily: plasmin; kringle homology (Tragments) #status experimental <PRO>
F;1-37,38-117,118-460/Product: plasminogen (fragment) #status experimental <PRO>
F;1-37/Domain: activation peptide (fragment) #status experimental <APT>
F;38-117,118-460/Product: plasmin (fragments) #status experimental <APT>
F;118-460/Product: miniplasminogen #status experimental <AMT>
F;118-460/Product: miniplasminogen #status experimental <MIN>
F;132-211/Domain: kringle homology <KR4>
F;236-460/Domain: kringle homology <KR4>
F;231-453/Domain: plasmin chain B #status experimental <BCH>
F;272,315,410/Active site: His, Asp, Ser #status predicted
complement factor I (EC 3.4.21.45) precursor - human N;Alternate names: C3b/C4b inactivator (.5species: Homo sapiens (man) (.5species: Homo sapiens (man) (.5species: Homo sapiens (man) (.5species: 31-Dec-1988 #text_change 09-3 (.5accession: A29154; A28434; $566420 R;Caccession: A29154; A28434; $566420 R;Catterall, C.F.; Lyons, A.;Sim, R.B.; Day, A.J.; Harris, T.J.R. Biochem, J. 242, 849-856, 1987 Biochem, J. 242, 849-856, 1987 A;Title: Characterization of the primary amino acid sequence of huma A;Reference number: A29154; MUID:87241401; PMID:2954545 A;Accession: A29154; MUID:87241401; PMID:2954545 A;Accession: A29154 A;Molecule type: mRNA A;Residues: 1-583 < CAT A;Residues: 1-583 < CAT A;Cross-references: UNIPROT:P05156; GB:Y00318 R;Goldberger, G.; Bruns, G.A.P.; Rits, M.; Edge, M.D.; Kwiatkowski, J. Biol. Chem. 262, 10065-10071, 1987
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Kwiatkowski,

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plasmin (EC 3.4.21.7) precursor [validated] - human N;Alternate names: plasminogen precursor [misnomer] N;Contains: angiostatin; microplasmin; plasminogen C;Species: Homo sapiens (man) plasmin; plasminogen C;Species: Homo sapiens (man) plasminogen (D;Pate: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004 C;Pate: 24-Apr-1984 #sequence revision 02-Dec-1994 $03735; A00929; A04627; C;Accession: A35229; IS242; A26646; I62738; I84609; S03735; A00929; A04627; R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4q24-4q25
C;Superfamily: human complement factor I; LDL receptor ligand-binding repeat homology;
C;Superfamily: human complement factor I; LDL receptor ligand-binding repeat homology;
C;Keywords: glycoprotein; hydrolase; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-335/Product: complement factor I heavy chain #status predicted <CFH>
F;291-255/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;259-293/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;340-583/Product: complement factor I light chain #status predicted <CFL>
F;340-583/Product: complement factor I light chain #status predicted <FL>
F;340-583/Domain: trypsin homology <TRY>
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C;Genetics:
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A;Cross-references: GB:J02770; NID:g182606; PIDN:AAA52455.1; PID:g182607
R;Ullman, C.G.; Haris, P.I.; Smith, K.F.; Sim, R.B.; Emery, V.C.; Perkins, S.J.
PEBS Lett. 371, 199-203, 1995
A;Title: beta-Sheet secondary structure of an LDL receptor domain from complement A;Reference number: S66420; MUID:95402210; PMID:7672128
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Similarity 30.0%; Pred. No. 2.5e-24;
33; Conservative 63; Mismatches 190; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEKPAEYS--SMVR--PICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRASKTHRYQ---IWTTVVDWIHPDLKR----IVIEYVDRIIFHENYNAGTYQNDIALIE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDCITGEDEVGCAGFASVAQEETEILTADMDAERRRIKSLLPK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YIDDRGFRYSDFTQWTAFLG-LHDQSQRSAFGVQERRLKRIISHFFFNDFTFDYDIALLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDCGDGSDEASC-----PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE
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J. Biol. Chem. 265, 6104-6111, 1990

A;Title: Characterization of the gene for human plasminogen, a key proenzyme in th A;Reference number: A35229; MUID:90202879; PMID:2318848

A;Accession: A35229

A;Molecule type: DNA

A;Residues: 1-810 <PET>
A;Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; GB:J05286; GB:A;Experimental source: leukocyte; lung fibroblast

A;Experimental source: leukocyte; lung fibroblast

R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A;Title: Definition of the transcription initiation site of human plasminogen gene A;Reference number: 152442; MUID:91097523; PMID:2268308

A;Accession: 152242
A;Molecule type: protein
A;Residues: 20-50,'Q','51-71,'B','73-85,87-100 <WI2>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment
A;Reference number: A04626; MUID:76043692; PMID:126863
A;Accession: A04626
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Eur. J. Biochem. 76, 129-137, 1977
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A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
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A;Accession: SU3,JJ
A;Molecule type: protein
A;Residues: 20-71,'E',73-76 <BRU>
A;Residues: 20-71,'E', 73-76 <BRU>
A;Residues: 20-71,'E', 73-76 <BRU>
A;Residues: 20-71, 'E', 73-76 <BRU>
A;Res
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R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 581-810 <WII>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
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R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human planareference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A04625; MUID:75093329; PMID:122932
A;Accession: A04625
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A; Residues: 292-471, 'D', 473-810 <MAL2>
A; Cross-references: GB: K02922, NID: 919
A; Accession: 184609
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A; Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810
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A;Residues: 367-419 <MAL3>
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A;Cross_references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
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A;Residues: 1-16 <MAL1>
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A;Reference number: A92048; MUID:69234739; PMID:4240117
A;Contents: annotation; active site
R;Trexler, M.; Vali, Z.; Patthy L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A;Reference number: A92382; MUID:82213905; PMID:6919539
A;Contents: annotation; omega-aminocarboxylic acid binding sites
R;Vali, Z.; Patthy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A;Reference number: A92458; MUID:85054794; PMID:6094526
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
R;Cao, Y.; Ji, R.W. Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferativ
A;Reference number: A58811; MUID:97067211; PMID:8910613
A;Contents: annotation
R;Lijnen, H.R.; Ugwu, F; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 (Martiotars. annotation and plasmino
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A; Residues: 483-507, 'E',509-604 <WI3>
R; Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A; Title: The primary structure of human plasminogen. II. Th.
A; Reference number: A92125; MUID:73149248; PMID:4694729
A; Contents: annotation; active site
R; Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A; Title: Studies on the active center of human plasmin. Par
                                                                                                                                                                                                                  A;Reference number: A58819; MUID:92031502; PMID:1657148
A;Contents: annotation
R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid A;Title: The refined structure of the epsilon-aminocaproic acid A;Reference number: A58818; MUID:92031503; PMID:1657149
A;Contents: annotation
R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the Brookhaven Protein Data Bank, December 1995 A;Reference number: A6524; PDB::ICBA A;Contents: annotation; X-ray crystallography, 2.1 angstroms, R;Tulinsky, A.; Mathews, I.I. submitted to the Brookhaven Protein Data Bank, December 1995 aubmitted to the Brookhaven Protein Data Bank, December 1995 A;Reference number: A65245; PDB::ICEB A;Contents: annotation; X-ray crystallography, 2.1 angstroms, R;Mullichak, A.M.; Tulinsky, A.; Ravichandran, K.G. Biochemistry 30, 10576-10588, 1991 A;Title: Crystal and molecular structure of human plasminogen A;Reference number: A58819; MUID:92031502; PMID::1657148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Contents: annotation; X-ray crystallography, R;Wu, T.P.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank, A;Reference number: A51911; PDB:1PKR A;Contents: annotation; X-ray crystallography, R;Padmanabhan, K.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank, A;Reference number: A52408; PDB:1PMK
                                                                                                         Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue
A;Reference number: A39483; MUID:92118803; PMID:1310033
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R;Stec, B.; submitted to
                             A; Contents: annotation; X-ray crystallography, R; Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano,
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C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately aft rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor, c;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial condict c;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Tog ting solid tumors.
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A; Contents: annotation; conformation by (1)H-NWR
C; Comment: Plasminogen is synthesized by the kidney and is present in plasma C; Comment: Plasminogen is converted to plasmin by plasminogen activators (see d) PIR:FGHUGB)
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F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;481-560/Domain: kringle homology <KR4>
F;475-352/Domain: kringle homology <KR4>
F;475-481/Domain: kringle homology <KR5
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A;Gene: GDB:PLG
A;Gross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; C;Function:
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A;Title: (1)H-NMR assignments and secondary structure of human plasminogen
A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
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                                                             252 ADSVLSLTFRSFDLASCDER-----GSDL-VTVYNTLSPME-----PHALVQLCGTY 297
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                                                                                                                                                                                                                                                    RAFQYHSKEQQCVIMAENRKSSIIIRMRDV---VLFEKKVYLSECKTGNGKNYRGTMSKT
                                                                                                                                                                                                                                                                                                              -SIPQHLVEEAERVMAEERVVMLPPRARSLKSFVVTSVVAFPTDSK---
                                                                                                                                                                                                                                                                                                                                                                            LDDYVNTQGASLFSVTKKQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
-RYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHA----HGYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 488; DB 1 24.5%; Pred. No. 4e-24; tive 103; Mismatches 2
                                                                                                                             GITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTD
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A; Molecule type: protein

A; Residues: 1-63,'T',65-416 < KAT>
A; Residues: 1-63,'T',65-416 < KAT>
A; Cross-references: UNIPROT: P00741

R; MCMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A; Title: The occurrence of beta-hydroxyaspartic acid in the A; Reference number: A20274; MUID: 83308813; PMID: 6688526

A; Recession: B20274

A; Molecule type: protein
A; Residues: 59-63,'X',65-69 < MCM>
R; Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
                                                                                                                                                                                                                                                                                      coagulation factor IXA (EC 3.4.21.22) precursor - bovine
N;Alternate names: Christmas factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A14757; B20274; I45891; A00923
R;Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.;
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A;Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas A;Reference number: A14757; MUID:80056619; PMID:291916
A;Accession: A14757
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A;Description: catalyzes the proteolytic activation of coagulation factor X in the preser A;Pathway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxysapartic acid; blood coagulation; calcium binding; carboxyglutami
F;1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
F;1-45/Domain: Gla domain homology (fragment) <GLA>
F;51-82/Domain: EGF homology <EGI>>
F;147-181/Domain: EGF homology <EGI>>
F;147-181/Domain: activation peptide #status experimental <APT>
F;182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;182-4409/Domain: EGF homology <EGI>>
F;182-4409/Domain: activation peptide #status experimental <AHC>
F;182-4409/Domain: trypsin homology <TRY>
F;18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide
F;53/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Cross-references: GB.J00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.;
J. Blochem. 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine
A;Reference number: A44556; MUID:89213999; PMID:3149637
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                                                    GVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIKENT
                                                                                                              NIFSKFGYGYVSGWGKVFNRGRSASILQYLKVPLVDRATCLRSTKFSIYSHMFCAGYHEG
                                                                                                                                                                  HVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSG
                                                                                                                                                                                                                                                                                      QSQRSAPGVQERRLKRIISHPFFNDF--TFDYDIALLELEKPAEYSSMVRPICLPDA--S
                                                                                                                                                                                                                                                                                                                                                GQFPWQVLLH----GETAAFCGGSIVNEKWVVTAAHC----IKPGVKITVVAGEHN
                                                                                                                                                                                                                                                                                                                                                                                                    GEWPWQVSLHALGQGHI----CGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHISKKLTRA--ETIFSNTNYENSSEAEIIWDNVTQSN-----QSFDEFSRVVGGEDAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTCTKHTYRCLNGLCLSKGNPECDGK-EDCSDGSDEKDCDCGLRSFTRQARVVGGTDADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CESNPCLNGGM-----CKDDINSYECWCQAGFEGTNCELDATCSIKNGRCK-QFCK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEFVRGNLERECKEEK-----CSFEEAREVFENTEKTTE--FWKQYVDGDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDYVEINGEKYCGERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFT
                                                                                                                                                                                                                               -TEKPEPTEQKRNVIRAIPYHSYNASINKYSHDIALLELDEPLELNSYVTPICIADRDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RDTDNKVVCS-----CTDGYRLAEDQK----SC-EPAVPFPCGRVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486; DB 1;
Pred. No. 2.5e-24;
9; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 416,
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WiAlternate names: plasminogen
(;Species: Bos prinigenius taurus (cattle)
C;Date: 30-Sep-1997 #sequence revision 28-Apr-1995
C;Accession: $45046; A25835; T45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.B.
submitted to the EMBL Data Library May 1994
A;Description: Cloning and characterizatin of the k
A;Reference number: $45046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 19q11-19q13.2
C;Superfamily: trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane
F;23-45/Domain: transmembrane #status predicted <TMN>
F;163-400/Domain: trypsin homology <TRY>
F;188-204,291-359,322-338,349-381/Disulfide bonds: #status pred
F;203,257,353/Active site: His, Asp, Ser #status predicted
κ;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, Eur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino soid soil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nepsin (EC 3.4.21.-) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Aug-2004
C;Accession: S00845
                                                                                              A;Cross-references: UNIPROT:P06868; EMBL:X79402; NID:g494962; PIDN:CAA55939.1; A;Experimental source: liver
                                                                                                                                                            A; Accession: S45046
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Leytus, S.P.; Loeb, K.R.; Hagen, Biochemistry 27, 1067-1074, 1988
                                                                                                                                      A; Residues: 1-812 <BER>
                                                                                                                                                                                                                                                                                                                                                                                             plasmin (EC 3.4.21.7) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:135685; OMIM:142440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: P05981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-417 < LEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S00845
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDSCQGDSGGPL---SSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWI 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDGKICTVTGWGNTQYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE--NLLPQQITPRMMCVGFLSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGVQERRLKRIISH----PFF--NDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPWQVSLRYDG-AHLCGGSLLSGDWVLTAAHCFPE----RNRVLSRWRVFAGA--VAQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --HTQRLLEVISV-----C----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKHTYRCLNGLCLSKGNPECDGKEDCSDGSD-EKDC-DCGLRSFTRQARVVGGTDADEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGDNSDEQ--GCSCPAQTF--RCSNGKCLSKSQQCNGKDD--CGDGSDEASCPKVNVVTC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDACQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHGLQ-LGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSSRSNARVAGLSCEEMGFLRALTHSELDVRTAGANGTSGFFC---VDEGRLP
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Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                             bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132;
                                                                                                                                                                                                                                   bovine
                                                                                                                                                                                                                                                                                                                        #text_change
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                                                                                                                                                                                                                                                                                                                          09-Jul-2004
                                            S.J.; Kampfer,
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       with
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       human
                                                                                                                 PID:g494
                                                 U.; Ric
    plasm
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a, rescription: dissolves the fibrin of blood clots; acts as a proteolytic factor in a ns the walls of the graafian follicle; also activates the urokinase-type plasminogen A, Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminocomic C; Keywords: duplication. fit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;27-812/Product: plasminogen #status experimental <PRO>
F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <APT>
F;104-583/Domain: plasmin chain A #status experimental <ACH>
F;104-583/Domain: kringle homology <KR1>
F;10-188/Domain: kringle homology <KR2>
F;382-359/Domain: kringle homology <KR3>
F;382-359/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR3>
F;384-805/Domain: kringle homology <KR5>
F;485-564/Domain: kringle homology <KR5>
F;584-802/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;584-805/Domain: trypsin homology <TRY>
F;565-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,331
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A;Residues: 706-741,'R',745-812 <MAL>
A;Residues: 706-743,'R',745-812 <MAL>
A;Residues: 706-743,'R',745-812 <MAL>
A;Residues: 706-743,'R',745-812 <MAL>
A;Residues: 706-743,'R',745-812 <MAL>
A;Birunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M., Bur, J. Biochem. 114, 465-470, 1981
ByTitle: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
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A; Residues: 27-334,'D', 336-515,'H',517-554,'L',556-812 <SCH>
R; Ralinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1994
A; Title: Characterization of a complementary deoxyribonucleic
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Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reference number: A25835; MUID:85203906; PMID:3846532
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                                                                                                                                                                                                                                                                                                                                                                       98 V--ILYEKRIYLLECKTGNGQTYRGTT----AETKSGVTCQKWS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AAVLIGLILVILGIGFLVWHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLAS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                               TNTERR-----HPGFEATFFQLPRMS----SCGGRLRKAQGT-------
                                                                                                                                                                                                                                                 SPEKFPLAGLEENYCRNPDNDENGP-----
                                                                                                                                                                                                                                                                                                              TTPGFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                AERVMABERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-----VKDALKLLYSGVPFL---GPYH-KESAVTAFSEGSVIAYYWSEFSIPOHLVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVVFLLLLFLKSGLG
PDGEPRPWCFTTDPQKRWEFCDIPRCTTPPPSSGPKYQCLKGTGKNYGGTVAVTESGHTC
                                                                                                                            CSGENYEGKIAKTMSGRDCQAWDSQSPHA----HGYIPSKFPNKNLKMNYCRN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNLAGRSVEDCAAKCEEETDFVCRAFQYHSKEQQCVVMAENSK-----NTPVFRMRD
                                                                                                                                                                                     GSDLV-TVYNTLS-----PMEPHALVQLCGTYP---PSYNLTFHSSQNVLLITLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 485.5; DB 1;
23.3%; Pred. No. 5.8e-24;
... Mismatches 340;
                                                                                                                                                                                                                                                                                                              -DSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDER----
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A;Note: parts of this sequence were determined R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A;Title: Prostasin is a novel human serine prot A;Reference number: A54866; MUID:94308140; PMID A;Accession: A54866
A;Molecule type: protein A;Residues: 45-64 <YUA>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A;Title: Molecular cloning, tissue-specific expression,
A;Reference number: A57014; MUID:95286644; PMID:7768952
A;Cross-references: GDB:676446; OMIM:600823
A;Map position: 16p11.2-16p11.2
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane
E;1-32/Domain: signal sequence #status predicted <SIG>
F;33-44,45-343/Product: prostasin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-343 <RES5
A;Cross-references: UNIPROT:Q16651; GB:L41351; NID:g862304; PIDN:AAC41759.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
A57014
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                                                                                                                           ;Gene: GDB:PRSS8
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A; Molecule type: protein
A; Residues: 20-25 < LIJ>
A; Residues: 20-848203
A; Molecule type: protein
A; Residues: 22-27 < LI2>
C; Comment: Plasminogen is
C; Comment: Plasminogen is
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A; Residues: 1-812 < DEGs-
A; Cross-references: UNIPROT: P20918; GB: J04766; NID: g200402;
A; Cross-references: UNIPROT: P20918; GB: J04766; NID: g200402;
R; Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Rur. J. Biochem. 224, 863-871, 1994
A; Title: Characterization of the murine plasma fibrinolytic
A; Reference number: S48202; MUID: 95010076; PMID: 7523120
A; Accession: S48202
A;Pathway: fibrinolysis
C;Superfamily: plasmin, kringle homology; plasminogen-related protein
C;Superfamily: plasmin; kringle homology; plasminogen-related protein
C;Seywords: angiogenesis inhibitor; blood; duplication; fibrinolysis;
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-812/Product: plasminogen #status predicted <PRO>
                                                                                                                                                                                                                                                                                                      C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin mediately after dissociation from the clot. In the presence of the inhibitor, the activation involves also removal of the activation peptide.

c;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. Togetil treating solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Contains: angiostatin; plasminogen (; Species: Mus musculus (house mouse) (; Species: Mus musculus (house mouse) (; Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 09-C; Accession: A38514; S48202; S48203 R; Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W. Genomics 8, 49-61, 1990 A; Schaefer (Characterization of the cDNA coding for mouse plasminogen A; Reference number: A38514; MUID:91184812; PMID:2081600 A; A; Accession: A38514; MUID:91184812; PMID:2081600
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F;45-343/Domain: prostasin heavy chain #status predicted <CHH>
F;45-281/Domain: trypsin homology <TRY>
F;35-341/Domain: transmembrane #status predicted <TMM1>
F;323-341/Domain: transmembrane #status predicted <TMM1>
F;37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted F;85,134,238/Active site: His, Asp, Ser #status predicted F;85,134,238/Active site: His, Asp, Ser #status predicted F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lasmin (EC 3.4.21.7) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALI----LQKGEIRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSWGDGCAGRNKPGVYTRLPLFRDWIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDACQGDSGGPL-SCPVEGLWYLTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTTCENLL-----PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLSRPITFSRYIRPICLPAANASPPNGLHCTVTGWGHV--APSVSLLTPKPLQQLEVPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAEGAEAPCGV---APQARITGGSSAVAGQWPWQVSITYEGV-HVCGGSLVSEQWVLSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -HKEAYEVKLGAH-QLDSYSEDAKVSTLKDIIPHPSYLQEGSQGDIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.3%;
                                                                                                                                                                                                               fibrin of blood clots; acts as a proteolytic factor in a varicallicle; also activates the urokinase-type plasminogen acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 483.5; DB 1
Pred. No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAA50168.1; PID:g200403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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                                                                                                                  precursor homology;
glycoprotein; hydro
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16-Aug-2004

serine

proteinase

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F;20-96/Domain: activation peptide #status predicted <APT>
F;79-466/Product: angiostatin #status predicted <AST>
F;79-581/S2-812/Product: plasmin #status predicted <MAT>
F;97-581/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;103-181/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR5>
F;881-560/Domain: kringle homology <KR5>
F;881-560/Domain: chain B #status predicted <BCH>
F;882-805/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <TRY>
F;497-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
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F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F;136,308/Binding site: carbohydrate (Asn) (covalent) #status pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;624,667,762/Active site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 FTTPGFPDSPY-----PAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                         WIK 850
                                                                                                                  MMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRD
                                                                                                                                                                                                                                                                                                                                                                                                                   RQARVVGGTDADEGEWPWQVSLHALGQG-HICGASLISPNWLVSAAHCYIDDRGFRYSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVEINGEKYCGERSOFVVTSNSNKITVRF---HS--DQSYTDTGFLAEYLSYDSSDPCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIPRCTTPPPPPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCK
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                                                                            ELCAGQLAGGVDSCQGDSGGPLVCFEKDKYIL-QGVTSWGLGCARPNKPGVYVRVSRFVD
                                                                                                                                                                            ACLESPNYMVADRTICYITGWGETQ
                                                                                                                                                                                                                       ICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENL--LPQQITPR
                                                                                                                                                                                                                                                                       EFYKVILGAHEEYIRGL-DVQEISVAKLILEP-----NNRDIALLKLSRPATITDKVIP
                                                                                                                                                                                                                                                                                                                     TQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRP
                                                                                                                                                                                                                                                                                                                                                                          - PGRVVGGCVANPHSWPWQISLRTRFTGQHFCGGTLIAPEWVLTAAHCL----EKSSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VNGPWCYTTNPRKLYDYCDIPLCASASSFEC-GKPQV----EPKKC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EASCPKVNVVTCTKHTYR-----CLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GDNSDEQG-----CSCPAQTFRC----SNGKCLSKSQQCNGKDDCGDGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYT--TDPSVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYQSDGQSYRGTSSTTITGKKCQSWAAMFPHRHSKTPENFPDAGLEMNYCRNPDGDKGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NLEENYCRNPDGETAPWCYTTDSQLRWEYCEIPSCESSASPDQSDSSVPPBEQTPVVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTTD--PDKRYDYCNIPECEEECMYCSGEKYEGKISKTMSGLDCQAWDSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGNGKDYRGKTAVTAAGTPCQGWAAQEPHRHSIFTPQTNPRADLEKNYCRNPD--GD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SPHA----HGYIPAKFPSKNLKMNYCHN-----PDGEPRPWCFTTDPTKRWEYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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26.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----CGGRLRKAQGTFN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----WEYC----NLKRCSETGGSVVELPTVSQEP-SGPSDSETDCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VPNNQHVKVRFKFFYLLEPGVPAGTCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 483.5; DB 1;
Pred. No. 7.8e-24;
6; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ser #status predicted
                                                                                                                                                                         -GTFGAGRLKEAQLPVIENKVCNRVEYLNNRVKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SPYYPGHYPPNIDCT
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                                                                                                                                                                                                                                                                                                                  plasmin (EC 3.4.21.7) precursor - rhesus macaque (.) Species: Macaca mulatta (rhesus macaque) (.) Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_chang (.) Accession: B32869; B30848 R. Tomlinson, J.E.; McLean, J.W.; Lawn, R.M. J. Biol. Chem. 264, 5957-5965, 1389 A; Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, A; Reference number: A32869; MUID:89174660; PMID:2925643
                                                                                                                  A;Residues: 1-810 <TOM>
A;Residues: 1-810 <TOM>
A;Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C;Keywords: plasminogen-related protein precursor homology <PLPH>
F;103-181/Domain: kringle homology
F;185-262/Domain: kringle homology
F;275-352/Domain: kringle homology
F;377-454/Domain: kringle homology
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Biochim. Biophys. Acta 1173, 350-352, 1993
A;Title: Cloning and sequence analysis of rat hepsin, a
A;Reference number: S33777; MUID:93305733; PMID:8318546
A;Accession: S33777
A;Accession: S33777
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                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: mRNA
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A; Residues: 1-416 < FAR>
                                                                                             F;1-9/Domain: signal sequence #status
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F;481-560/Domain: kringle homology <KR5>
F;581-003/Domain: trypsin homology <TRY>
F;49-73.53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                   DIALLKLSSPAIITDKVIPACLPSPNYVVADRTECFITGWGETQ-GTYGAGLLKEARLPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALVQLCGTYP---PSYNLTFHSSQNVLLITLITNTERR-----HPGFEATFFQLPRMS- 338
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      GCARPNKPGVYVRVSRFVTWIE
                                                         GCAGRNKPGVYTRLPLFRDWIK 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTGTPCQEWAAQEPHSHRIFTPETNPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLFDYCD
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                                                                                                                      IENKVCNRYEFLNGTVKTTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYIL-QGVTSWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RTPENFPCKNLDENYCRNPDGEKAPWCYTTNSQ----VRWEYCKIPSCESSPVSTEP 361
                                                                                                                                                                             INQTTCE--NLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGD 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----WHEKTPENFPNAGL----TMNYCRNPDADKGPWCFTTDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FHSD-QSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 477; DB 2;
Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 288; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EECAAKCEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KDDC--GDGSDEASCPKVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SSTTTTGK----KC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;142-180/Domain: EGF homology <EGF>
F;184-293/Domain: C17/C18 repeat homology <CTR2>
F;380-361/Domain: Complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;445-679/Domain: trypsin homology <TRY>
F;445-679/Domain: trypsin homology <TRY>
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,996-90,142-156,152-165,164-211,164-211,241-259,300-348,328-361,366-412,396-430,434-552,996-90,142-156,152-165,164-211,241-259,300-348,328-361,366-412,396-430,434-552,996-90,142-156,152-165,164-211,241-259,300-348,328-361,366-412,396-430,434-552,996-90,142-156,152-165,164-211,241-259,300-348,328-361,366-412,396-430,434-552,996-90,142-156,152-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165,164-165
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R;Thiel, S.; Vorup-densen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.;
Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that
A;Reference number: A59271; MUID:97242412; PMID:9087411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homok C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine pi F;1-15/Domain: signal sequence #status predicted <SIG> F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT> F;19-134/Domain: C1r/C1s repeat homology <CIRI> F;19-134/Domain: C1r/C1s repeat homology <CIRI> F;19-134/Domain: C1r/C1s repeat homology <CIRI>
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N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:MASP2
A;Cross-references: GDB:6071500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:O00187; GB:Y09926; NID:g4007
A,Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1p36.2-1p36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A59271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   412
                                                                                                                                                                             321
                                                                                                                                                                                                                                      467
                                                                                                                                                                                                                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                             202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
      GLCLSKGNPECDGKEDC-SDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --VLATICGQESTDTERAPGKDTFYSLGSSLDTTFRSDYSNEKPFTGFEA-FYAAEDIDE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHALVOLCG----TYPPSYNLTFHSSQNVLLITLITNTERRHP--GFEATFFQLPRMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPME 286
                                                                                                                   SCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHT-----YRCLN
                                                                                                                                                                                                                                                                                                KTLPHRIETKSNTVTITFVTDESGDHTGWKIHYTSTAHACPYPMAPPNGHVSPVQAKYIL
                                                                                                                                                                                                                                                                                                                                                ERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP-----GQFTCRTGRCIR
                                                                                                                                                                                                                                                                                                                                                                                                             PRPYPKLSSCTYSISLEEGFSVILDFVESFDVETH-PETLCPYDFLKIQTDREEHGPFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEK-----YCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQVAPGEAPTCDHHCHNHLGGFYCSCRAGYVLHRNKRTCSALCSGQVFTQRSGELSSPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLASPGFP-GEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAK---
                                                                                                                                                                                                                                KELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQ----GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.1%; Score 475; DB 1; 25.4%; Pred. No. 2.3e-23;
                                                                                                                                                                             DSFSIFCETGYELLQGHLPLKSFTAVCQK----DGSWDRPMPAC
                                                            ------DCGP-PDDLPSGRVEYITGPGVTTYKAVIQYSCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not shown; not compared with
      --SDEKD---CD--CGLRSFTRQARVVGGTDADEGE 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID: g4007626; PIDN: CAA71059.1; PID: g400767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGRLRKAQGTFNSPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conceptual
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                                                                                                                                                                                361
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A; Bulecule type: LANS A; Reddues: 1-461 (ANS) A; Residues: 1-461 (ANS) A; Cross-references: GB:KO2048 R; Redden: A; Cross-references: A30511; MUID:88327116; PMID:3416069 A; Accession: A30511; MUID:88327116; PMID:3416069 A; A; Residues: 8-24 (REI) A; Robert R; Koeberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S. AM. J. Hum. Genet. 45, 448-457, 1989 A; Title: Functionally important regions of the factor IX gene have a low A; Reference number: A32989; MUID:89371752; PMID:2773937 A; Recession: A32989 A; Status: not compared with conceptual translation A; Residues: 30-92 (KOS) A; Reference number: A32989 A; Residues: 30-92 (KOS) R; Molecule type: DNA A; Residues: 30-92 (KOS) R; Lundblad, R.L.; Roberts, H.R.; Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985 A; Title: Evidence for a prevalent dimorphism in the activation peptide o: A; Reference number: A22673; MUID:85190593; PMID:3857619 A; Accession: A22673
A; Molecule type: mRNA A; Residues: 1-193, 'T', 195-461 (MCG) A: Cross-references: CR:M11309; MID:6180552; PIDN:AAA52023.1; PID:g180553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P00740; GB:K02402; NID:g182612; PIDN:AAB59620.1; PID:g182613 R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Brd EMBO J. 3, 1053-1060, 1984

A;Title: The gene structure of human anti-haemophilic factor IX.

A;Reference number: A37570; MUID:84236100; PMID:6329734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human N;Alternate names: antihemophilic factor B; Christmas factor C;Species: Homo sapiens (man) C;Pate: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004 C;Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; R;Coshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K. Biochemistry 24, 3736-3750, 1985 A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic A;Paccession: A00922; MUID:86000558; PMID:2994716
   A;Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553 A;Note: the authors translated the codon ACA for residue 29 as Tyr R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Finde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-461 < Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-461 <YOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INYIPWIE 680
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                                                                                                                                                                                                                                                                                                                                                                                                                          the factor IX gene have a low rate PMID:2773937
                                                                                                                                                                                                                                                                          Roberts, H.R.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g4469253
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            Findeli,
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            Tolstosh
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A; Ctoflet, E.
                                                                                                                                                                                       A;Reference number:
A;Accession: I59612
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                                                                                                                          A; Molecule type:
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A;Note: processed forms expressed in recombinant system R;Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Bee EMBO J. 9, 475-480, 1990
A;Title: The first EGF-like domain from human factor IX A;Reference number: S12377; MUID:90151623; PMID:2406129 A;Accession: S12377
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A;Residues: 47-52, XX',55-60, 'X',62, 'XX',65 <THA>
R;Residues: 47-52, XX',55-60, 'X',62, 'XX',65 <THA>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the A;Teference number: A20274; MUID:83308813; PMID:6688526
A;Accession: A20274
A; Residues: 444-461 <RES>
A; Cross-references: GB:S66752; NID:g439773;
R; Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.;
Science 239, 491-494, 1988
                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 92-130 < HAN
A; Residues: 92-130 < HAN
A; Note: NMR detection of calcium binding by
R; de la Salle, C.; Charmantier, J.L.; Baas,
Thromb. Haemost. 70, 370-371, 1993
A; Title: A deletion located in the 3' non tr
A; Reference number: 159612; MUID: 94054330; F
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EMBO J. 9, 3295-3301, 1990
A;Tille: Characterization of recombinant human Factor IX
A;Reference number: S12058; MUID:91006024; PMID:2209546
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A;Residues: 105-109, 'Ill-115 < MCM'>
A;Residues: 105-109, 'T.; Carvallo, D.; Cordier, P.; Ulrich,
R;Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich,
Eur. J. Biochem. 172, 565-572, 1988
Eyr. J. Biochem. 172, 565
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A;Title: Development of an immunoaffinity process for factor IX pu A;Reference number: A60486; MUID:90194857; PMID:2316207
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A;Residues: 1-12,'S',14-73,'P',75-82,'K',84-203,'P',205-216,'G',218-298,'A',299-356,'A',2
A;Croos-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
A;Experimental source: liver
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Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A;Title: Incolation and characterization of a cDNA coding
A;Reference number: A30623; MUID:83065193; PMID:6959130
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A;Title: Isolation and characterization of human factor IX
A;Reference number: A37546; MUID:84300526; PMID:6089357
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A;Residues: 1-193,'T',195-461 <JAY>
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1;
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1;
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A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-bas A;Reference number: A21337; MUID:83220788; PMID:6687940
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A;Residues: 38-193,'T',195-326 <JAG>
A;Cross-references: GB:M35672
                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDB
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; PMID:8236150
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M.J.; Schwartz, A.;
                                            PIDN:AAB28588.1; PID:g439774 Sommer, S.S.
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A.; Beesley,
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Warren, S.T.
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A;Reference number: A30622; MUID:99078229; PMID:2592173

A;Contents: annotation; sequence of mutant B(M) Nagoya

A;Note: carboxylation, glycosylation, and cleavage sites

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Baron, M; Norman, D.G; Harvey, T.S; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle

R;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, vitamin R

C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc

C;Genetics:

A;Gene: GDB:F9

A;Cross-references: GDB:119900; OMIM:306900

A;Map position: Xq27.1-Xq27.2

A;Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1

C;Function:

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C;Superfamily: coagulation factor #status predicted <SIG>

F;29-46/Domain: signal sequence #status predicted <SIG>

F;24-46/Domain: signal sequence #status predicted <SIG>
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R;MOTITA, T.; IBacc...
J. Biol. Chem. 260, 2583,
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A;Contents: annotation; calcium binding, correction
A;Contents: annotation; calcium binding, correction
R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A;Title: Defective propeptide processing of blood clotting factor
A;Reference number: A37545; MUID:86189947; PMID:3009023
A;Contents: annotation; signal sequence cleavage site
R;Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu,
J;Biol. Chem. 264, 21257-21265, 1989
A;Title: Blood clotting factor IX B(M) Nagoya: substitution of arg
A;Reference number: A3622; MUID:90078229; PMID:592373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623
R;Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw Biochemistry 33, 5167-5171, 1994
A;Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin A;Reference number: A54255; MUID:94227047; PMID:8172892
A;Accession: A54255
A;Molecule type: protein
A;Residues: 'D',204,'X',206-211;212,'D',214,'X',216-221,'D' <AGA>
A;Molecule type: protein
A;Residues: 'D',204,'X',206-211;212,'D',214,'X',216-221,'D' <AGA>
A;Note: the residues designated 'X' were determined to be threonine bound to carbohydrat A;Note: the residues designated 'X' were determined to be threonine bound to Carbohydrat Cin. Invest. 61, 1528-1538, 1978
J. Clin. Invest. 61, 1528-1538, 1978
                                                                                                                                                                                                 F;29-46/Domain: propeptide #status experimental <PPT>
F;31-91/Domain: Gla domain homology <GLA>
F;47-191/Product: coagulation factor IXa light chain #status experimental
F;47-128/Domain: EGF homology <EG1>
F;134-170/Domain: EGF homology <EG2>
F;134-170/Domain: EGF homology <EG2>
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J. Biol. Chem. 259, 5698-5704, 1984
A;Title: Derivatives blood coagulation factor IX contain a high affinity Ca2+-binding A;Fitle: number: A37543; MUID:84185715; PMID:6425296
A;Contents: annotation; calcium binding
A;Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
F;192-226/Domain: activation peptide #status experimental <ACT>
F;297-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;227-454/Domain: trypsin homology <TRY>
F;53,54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid
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A;Reference number: A18483; MUID:78194509; PMID:659613
A;Contents: annotation; activation; active site; carbohydrate binding
A;Contents: Annotation; Activation; C.M.; Graham, J.B.; Roberts, H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Genomic amplification with transcript sequencing A; Reference number: I59529; MUID:88127096; PMID:3340835 A; Accession: I59529
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A; Note: 194-Thr was also found
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C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text
C;Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text
C;Accession: A27431, A00920; A37940
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Biochemistry 26, 7221-7228, 1987
A;Title: Organization of the gene for human factor XI.
A;Reference number: A27431; MUID:88107663; PMID:2827746
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-625 < ASSA>
A; Cross-references: UNIPROT: P03951; GB: M18295
A; Note: the sequence shown follows the authors'
R; Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.;
Biochemistry 25, 2417-2424, 1986
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A; Molecule type:
A; Residues: 1-62
A; Cross-reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human N; Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
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                                                                                                      A; Title: Amino acid sequence of human factor XI, a blood A; Reference number: A00920; MUID:86243360; PMID:3636155
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                                                                                  A; Accession: A00920
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     ;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
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                              type: mRNA
1-625 <FUJ>
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Pred. No. 1.6e-23;
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June

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A; Map position: 435.4435
A; Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
C; Munction: catalyzes the proteolytic activation of coagulation factor IX
A; Pathway: blood coagulation intrinsic pathway
C; Superfamily: coagulation factor XI; trypsin homology
C; Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-387/Product: coagulation factor XIa heavy chain #status experimental <HCH>
F; 19-108/Domain: apple repeat <AP1>
F; 109-128/Domain: apple repeat <AP2>
F; 199-288/Domain: apple repeat <AP3>
F; 290-379/Domain: apple repeat <AP3>
F; 388-618/Domain: trypsin homology <TRY>
F; 381-618/Domain: interchain #status experimental
F; 46-76, 50-56, 110-193, 136-165, 140-146, 200-283, 226-255, 230-236, 291-374, 317-346, 321-327, 38
F; 397-Disulfide bonds: interchain #status predicted
F; 387-388/Cleavage site: Arg-11e (coagulation factor XIIa) #status experimental
F; 431, 480, 575/Active site: His, Asp, Ser #status predicted
F; 491/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 441/Binding site: carbohydrate (Asn) (covalent) #status experimental
trypsin (EC 3.4.21.4) precursor - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_cl C;Accession: S40007 R;Mueller, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 28-33;35-49; X',51-55; X',57-63;70-75; X',77-79;107-109; X',111-112;132-139;
A; Residues: 28-33;35-49; X',51-35; X',318-319;320-326; X',328-330; X',347-349;377, X',375
C; Comment: The proenzyme consists of two identical chains linked by one or more disulfid neactive site, and a heavy chain, which associates with high molecular weight (HMW) kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;McMullen, B.A.; Fujikawa, K.; Davie, E.W. Biochemistry 30, 2056-2060, 1991 Biochemistry 30 of the disulfide bonds in A;Title: Location of the disulfide bonds in A;Reference number: A37940; MUID:91152017; FA;Accession: A37940
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A;Map position: 4q35-4q35
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2;
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A;Gene: GDB:F11
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Best Local S
Matches 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 SDEASCPKV--NVVTCTKHTYRCLNGLCLSKGNPECDGKEDC-----SDGSDEK-----
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                                                                                                                                                                                                                                                                                                                                                                                          LQKAKIPLVTNEECQKRYRGHKITHKMICAGYREGGKDACKGDSGGPLSC--KHNEVWHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKMAESGYDIALLKLETTVNYTDSQRPICLPSKGDRNVIYTDCWVTGWGYRKLRDKIQNT
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                                                                                                                                                                                                                                                                           VGITSWGEGCAQRERPGVYTNVVEYVDWILEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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PMID:1998667
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F;1-96/Domain: plasminogen-related p.
F;103-181/Domain: kringle homology </br>
F;185-262/Domain: kringle homology </br>
F;275-352/Domain: kringle homology </br>
F;275-352/Domain: kringle homology </br>
F;379-456/Domain: kringle homology </br>
F;482-561/Domain: kringle homology </br>
F;582-803/Domain: trypsin homology </br>
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C;Species: Er
C;Date: 21-Fe
C;Accession:
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A;Accession: S40007
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <MUE>
A;Cross-references: UNIPROT:P35037; EMBL:Z22930; NID:g410323
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;49-269/Domain: trypsin homology <TRY>
F;89,134,230/Active site: His, Asp, Ser #status predicted
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A;Cross-references: UNIPROT:(029485; EMBL:U33171; NID:g1046360; PID:g1046361
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precu
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: I46260
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights: A;Reference number: 146259; MUID:96025778; PMID:7592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I46260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lasmin (EC 3.4.21.7) precursor - western European hedgehog;Species: Erinaceus europaeus (western European hedgehog);Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_cha;Accession: I46260
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                                                                                                                                                                                    Similarity
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                                     GQFTCRTGRCIRKEL----RCDGWADCTDHSDE--
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                                                                                                                         NGEKYCGERSQFVVTSNSNKITVRFHSDQS
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                                                                             NGEHYQGN-----VAVTVSGLTCQRWGEQSPHRHDRTPENYPCKNLDENYCRNPDGEPAP
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ni kringle homology <KR2>
ni kringle homology <KR3>
ni kringle homology <KR3>
ni kringle homology <KR4>
ni kringle homology <KR5>
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TNSSVRWEFCKIPDCVSSASETEHSDAPVIVPPEQTPVVQECYQGNGQTYRGTS
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                                                                                                                                                                   62;
                                                                                                                                                                                    Score 468; DB 2
Pred. No. 8e-23;
                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              precursor homology
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                                                                                                                       YTDTGFLAEYLSYDSSDPCP
                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of hedgehog
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                                                                                                                                                              Gaps
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391
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and-binding repeat and-binding r	al translation D:g984320; PIDI [-binding repeat leat homology <	RESULT 29 A57096 A57096 A57096 nudel protein precursor - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004 C;Accession: A57096 R;HOng, C.C.; Hashimoto, C. Cell 82, 785-794, 1995 A;Title: An unusual mosaic protein with a protease domain, encoded by the nudel gene, is A;Reference number: A57096; MUID:95401268; PMID:7671306 A;Accession: A57096	Qy 712 IALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVI 771	Qy 495TCKNKFCKPLFWVCD-SVNDCGDNSDEQGCSCPAQTFR 531
RESULT 30 A30351 Coagulation factor IXa (BC 3.4.21.22) precursor - dog C;Species: Canis lupus familiaris (dog) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A30351; I46201 R;Evans, J.P.; Watzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A. Blood 74, 207-212, 1989 A;Title: Molecular cloning of a cDNA encoding canine factor IX. A;Reference number: A30351; MUID:89323338; PMID:2752110 A;Accession: A30551 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-452 <eva> A;Residues: 1-452 <eva> A;Cross-references: UNIPROT:P19540; GB:M21757; NID:g972719; PIDN:AAA75006.1; PID:g163948</eva></eva>	OY 735 ASHVEPAGKAIW		QY 476 DCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGC-SCPAQTFRC	Qy 205 TVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTF 260

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YSSMVRPICLPD 734
:: |:|||||
PNRWVKPICLPD 1256
                                                                                                        WGDGCAGRNKP 836
|:||| :
|HGNGCARPQEF 1365
                                                                                                                                        SCPAQTFRC-- 532
| ; |
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R;Axelrod, J.H.; Read, M.S.; Brinkhous, K.M.; Verma, I.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 5173-71, 1990

A;Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic A;Reference number: 146201; MUID:90311364; PMID:2367529

A;Reference number: 146201

A;Reference number: 146201

A;Reference number: 146201

A;Reference number: 145201

A;Rolecule type: mRNA

A;Residues: 1-452 <AXE>

A;Cross-references: GB:M33826; NID:g163949; PIDN:AAA30844.1; PID:g163950

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C;Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-40/Domain: propeptide #status predicted <PRO>

F;41-452/Product: coagulation factor IX #status predicted <MAT>
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F;121-136/Domain: EGF homology <EGI>
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F;218-445/Domain: EGF homology <EGI>
F;218-445/Domain: EGF homology <EGI>
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F;318-445/Domain: EGF homology <EGI>
F;358-306,402/Active site: His, Asp, Ser #status predicted

A;57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di

F;55-62,90-104,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di

F;55-62,90-104,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di

F;55-62,90-104,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di

F;55-62,90-104,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di
Search completed: November 29, 2004, 08:33:30 Job time: 39.6873 secs
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1: /cgn2 6/ptcdata/2/pubpaa/US07 PUBCOMB.pep:*

3: /cgn2 6/ptcdata/2/pubpaa/PCT NEW PUB.pep:*

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US-10-295-027-1185
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US-10-099-700A-2
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Sequence 418, Appli
Sequence 418, Appli
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Sequence 169, Appli
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APPLICANT: MACKA, DAVID A.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Composit
TITLE OF INVENTION: Methods of Screening for Modulators of
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PILING DATE: 2002-02-13
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                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1185
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US-10-295-027-1185
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APPLICANT: Aziz, Natash
APPLICANT: Ginsberg, Wer
APPLICANT: Gish, Kurt C
APPLICANT: Glynne, Riche
APPLICANT: Hevezi, Peter
APPLICANT: Mack, David I
                                                                                                                           Remaining Prior Application
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1185
LENGTH: 855
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Best Local Similarity
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Gish, Kurt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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                           Score 4659; D. Pred. No. 0; O; Mismatches
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           US-10-072-012-353
, Sequence 353, Application US/10072012
Publication No. US20040033493A1
; GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Serhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Patturajan, Meera
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR APPLICATION NUMBER: 60/266,406
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US-10-072-012-353
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Best Local
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APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids
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TYPE: PRT
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OR APPLICATION NUMBER: 60/266,767

OR FILING DATE: 2001-02-07

OR PILION DATE: 2001-02-07

OR FILING DATE: 2001-02-07

OR APPLICATION NUMBER: 60/266,975

OR APPLICATION NUMBER: 60/266,975

OR FILING DATE: 2001-02-07

OR FILING DATE: 2001-02-07
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Grosse, William M.
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Pena, Carol B. A
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Taupier Jr, Raymond
Gusev, Vladimir Y.
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                                                                                                                               PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYT
                                                                                                                                                   PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
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                                                                                                                                                                                                                            AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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                                                                RLPLFRDWIKENTGV
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Sequence 412, Applic Publication No. US20 GENERAL INFORMATION: GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar APPLICANT: CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102 APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258 APPLICANT: Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P. Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Graupier Jr, Raymond J. Spytek, Kimberly Zerhusen, Bryan Patturajan, Meera Shimkets, Richard Application US/10072012 o. US20040033493A1

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; SOFTWARE: PatentIn Ver.; SEQ ID NO 412
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
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DR FILING DATE: 2001-01-31
DR APPLICATION NUMBER: 60/266,406
DR FILING DATE: 2001-02-02
DR APPLICATION NUMBER: 60/266,767
DR FILING DATE: 2001-02-05
DR APPLICATION NUMBER: 60/267,057
DR APPLICATION NUMBER: 60/267,057
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DR APPLICATION NUMBER: 60/267,057
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PRILING DATE: 2001-01-31

DR FILING DATE: 2001-01-31

DR APPLICATION NUMBER: 60/265,517

DR APPLICATION NUMBER: 60/265,517

DR FILING DATE: 2001-01-31

DR APPLICATION NUMBER: 60/265,412

DR FILING DATE: 2001-01-31
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APPLICATION NUMBER: 60/267,459
FILING DATE: 2001-02-08
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                                                                                 SDELNCSCDAGHQFTCKNKFCKFLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
                                                                                                     SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
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DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
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Pred. No. 0;
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Sequence 419, Application US/10
Publication No. US/20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Sertusen, Bryan
APPLICANT: Stimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Gangolli, Esha
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muralidhe
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Golman, Steven D.
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                                                                                     PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Alsobrook II, John P.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Aci
FILS REPERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
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APPLICATION NUMBER: 60/267,459 FILING DATE: 2001-02-08
                                               APPLICATION NUMBER: 60/266,975 FILING DATE: 2001-02-07
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Taupier Jr. Raymond of
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
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Padigaru, Muralidha
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
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Zerhusen, Bryan
Teruraian, Meera
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D. US20040033493A1
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Proteins and Nucleic Acids
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; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 419
; LENGTH: 855
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                                                                                                      AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
                                                                                                                      AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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                  RLPLFRDWIKENTGV
                                                                   PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
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 RLPLFRDWIKENTGV
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                                                   PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYT
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Pred. No. 0;
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APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INUMINION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,406
PRIOR FILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
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Sequence 354, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
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                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-354
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Best Local S
Matches 851
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 354
LENGTH: 855
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RFILING DATE: 2001-02-02
DR APPLICATION NUMBER: 60/266,767
DR FILING DATE: 2001-02-05
DR APPLICATION NUMBER: 60/267,057
DR FILING DATE: 2001-02-07
DR FILING DATE: 2001-02-07
                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/267,459 FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/266,975
FILING DATE: 2001-02-07
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                    VLIGLLLVLLGIGFLVMHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKV
                                                                             VLIGLLLVLLGIGFLVMHLQYRDVRVQKVFNGYWRITNENFVDAYENSNSTEFVSLASKV
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Gerlach, Valerie
Taupier Jr. Raymond of Guser, Vladimir Y.
Colors
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Grosse, William M.
Alsobrook II, John P.
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Rastelli, Luca
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Patturajan, Meera
Shimkets, Richard
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; Pred. No. 0;
0; Mismatches
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Sequence 420, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Settusen, Bryan
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Gangolli, Esha
APPLICANT: Gangolli, Esha
APPLICANT: Anderson, David W.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
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APPLICANT: Furtak, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Catherine B.
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-07
PRIOR PRILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/267,459
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 420
LENGTH: 855
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Best Local Similarity
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APPLICANT: Anderson, David W
APPLICANT: Paddigaru, Muralidhara
APPLICANT: Paddigaru, Muralidhara
APPLICANT: Paddigaru, Muralidhara
APPLICANT: Miller, Charles B
APPLICANT: Miller, Charles B
APPLICANT: Miller, Charles B
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Aci
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT APPLICATION NUMBER: 60/260,018
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR APPLICATION NUMBER: 60/272,411
                                                                                                                                                                                                                                    APPLICANT Kekuda, Ramesh APPLICANT Alsobrook II, J APPLICANT Alsobrook II, J APPLICANT Liu, Xiaohong APPLICANT Liu, Xiaohong APPLICANT Grosse, William APPLICANT Grosse, William APPLICANT Lepley, Denise APPLICANT Lepley, Denise APPLICANT Gorman, Linda APPLICANT Gorman, Linda APPLICANT Gorman, Karen APPLICANT Bilerman, Karen APPLICANT Bilerman, Karen APPLICANT Rothenberg, Mar APPLICANT Schore, David J APPLICANT Schore, Mar APPLICANT Schore, Sweeth APPLICANT Schore, David APPLICANT Schore, David J APPLICANT Schore, Schores APPLICANT Rothenberg, Mar APPLICANT Schore, Schores APPLICANT Schore, Schores APPLICANT Rothenberg, Maral Rothenbe
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Gorman, Linda
Edinger, Shlomit F
Sciore, Paul
Ellerman, Karen
Malyankar, Uriel W
Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
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Tchernev, Velizar T
Liu, Xiaohong
Spytek, Kimberly A
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Grosse, William M
Lepley, Denise M
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Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                          Shenoy, Suresh G
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PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR PILING DATE: 2001-07-05
PRIOR PILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
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US-10-037-417-132
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                                                                   DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
                                                                                                                              DCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLISPNWLVSAAHCYID
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                                  DRGFRYSDPTQWTVFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
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Pred. No. 0;
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APPLICANT: Edgar O. Ong
APPLICANT: Edgar O. Ong
APPLICANT: Edgar O. Ong
APPLICANT: Jiunn-Chern Yeh
APPLICANT: Jiunn-Chern Yeh
APPLICANT: Jiunn-Chern Yeh
APPLICANT: Jiunn-Chern Yeh
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: METHODS BASED THEREON
FILE REFERENCE: 24745-1607
CURRENT APPLICATION NUMBER: US/09/776,191
CURRENT APPLICATION NUMBER: 60/213,124
PRIOR APPLICATION NUMBER: 60/213,124
PRIOR APPLICATION NUMBER: 60/234,840
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/13,542
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/657,968
PRIOR PILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 2
LENGTH: 855
TYPE: PRT
ORGANISM: Homo Sapien
US-09-776-191-2
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Publication No. US20030119168A1
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Local Similarity 99.5%;
nes 851; Conservative
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Pred. No. 0;
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                                                                                                                      Query Match
Best Local Similarity 99.0
851; Conservative
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APPLICANT: Edwin I. Madison
APPLICANT: Edgar O. Ong
APPLICANT: Edgar O. Ong
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7,
TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: 24745-1613
CURRENT APPLICATION NUMBER: US/10/099,700A
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/275,592
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 22
SOPTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 855
TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                     1 MGSDRARKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA
DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
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Pred. No. 0;
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APPLICANT: MODISON: Edwin
APPLICANT: Ong, Edgar
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A
ITITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASE 20,
ITITLE OF INVENTION: METHODS BASED THEREON
FILE REFERENCE: 24745-1618
CURRENT APPLICATION NUMBER: US/10/190,030B
CURRENT FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 24
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 855
TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                    RESULT 10
US-10-190-030B-2
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              US-10-190-030B-2
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Best Local S
Matches 851
Sequence 2, Application US/10302840A
Publication No. US20030134794A1
GENERAL INFORMATION:
APPLICANT: Madison, Edwin L.
APPLICANT: Ong, Edgar O.
APPLICANT: Ong, Edgar O.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE CVSP17,
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; TITLE OF INVENTION: POLYPEPTIDES AND METHODS
; FILE REFERENCE: 24745-1622
; CURRENT APPLICATION NUMBER: US/10/302,840A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/332,015
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-302-840A-2
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                     PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
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FILE REFERENCE: 24745-1621

CURRENT APPLICATION NUMBER: US/10/267,219

CURRENT FILING DATE: 2002-10-08

PRIOR APPLICATION NUMBER: 60/328,530

PRIOR FILING DATE: 09-OCT-2001

NUMBER OF SEQ ID NOS: 18

SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 855

TYPE: PRT

ORGANISM: Homo Sapien

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Publication No. US20030143219A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 851; Conserv
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APPLICANT: Yeh, Jiunn-Chern
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE
TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
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Sequence 2, Application US/10112221A

Publication No. US20030166851A1

GENERAL INFORMATION:

APPLICANT: Madison, Edwin

APPLICANT: Ong, Edgar O.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 9

TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON

FILE REFERENCE: 24745-1615

CURRENT APPLICATION NUMBER: US/10/112,221A

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: 60/279,228

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-05-15

NUMBER: OF SEQ ID NOS: 22

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 855

TYPE: PRT

ORGANISM: Homo Sapien
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US-10-112-221A-2
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Publication No. US20030181658A1

GENERAL INFORMATION:

APPLICANT: Madison, Edwin

TITLE OF INVENTION: POLYPETIDES AND METHODS SERINE PROTEASE CVSP14, THE ENCODING SERING PROTEASE CVSP14, THE ENCODING SERING SE
                                                                                                                                                                                                                                                                                        Matches
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                                                                                              VLIGLLLVLLGIGFLVWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV
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Sequence 2, Application US/10147211A

Publication No. US20030235900A1

GENERAL INFORMATION: Edward

APPLICANT: Madison, Edward

APPLICANT: Yeh, Jiumn-Chern

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERITILE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON

FILE REFERENCE: 24745-1616

CURRENT APPLICATION NUMBER: US/10/147,211A

CURRENT APPLICATION NUMBER: US/291,001

PRIOR APPLICATION NUMBER: 60/291,001

PRIOR APPLICATION NUMBER: 60/291,001

PRIOR FILING DATE: 2001-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH. 05E
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US-10-147-211A-2
 Query Match
                             -10-147-211A-2
                                                       LENGTH: 855
TYPE: PRT
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                                                       Sequence 2, Application US/10156214A Publication No. US20040001801A1 GENERAL INFORMATION:
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APPLICANT: Edwin L. Madison
APPLICANT: Joseph Edward Semple
APPLICANT: George P. Vlasuk
APPLICANT: Scott Jeffrey Kemp
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TITLE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic
TITLE OF INVENTION: Thereof
FILE REFERENCE: 24745-1611
CURRENT APPLICATION NUMBER: US/10/156,214A
CURRENT FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 611
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Matches 851; Conservative
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TYPE: PRT
ORGANISM: Homo Sapien
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                                                  AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: 60/265,514
PRIOR PPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
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PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/267,057
                                                                             ; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-352
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                                                                                                                                                         Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 352
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Publication No. US200400334937
GENERAL INFORMATION:
APPLICANT: Tcherney, Velizar
APPLICANT: Spytek, Kimberly
  Matches 851;
                                     Query Match
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PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
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Gerlach, Valerie
Taupier Jr, Raymond of Gusev, Vladimir Y.
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Rieger, Daniel K.
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Grosse, William M.
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Rastelli, Luca
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Shimkets, Richard
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Sequence 411, Application US/100, Publication No. US20040033493A1; GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar APPLICANT: Spytek, Kimberly APPLICANT: Syytek, Kimberly Zerhusen, Bryan APPLICANT: Patturajan, Meera APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha APPLICANT: Padigaru, Muralidha;
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US-10-072-012-411
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APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Wolenc, Adam R.
APPLICANT: Wolenc, Adam R.
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Alsobrook II, John P.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine B.
TITLE OF INVENTION: Proteins and Nucleic Acids Enception Control of the Policant Application NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: US/10/258102
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PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-31
PRIOR PELLING DATE: 2001-01-31
PRIOR PELLING DATE: 2001-01-31
PRIOR PELLING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/266,395
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
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PRIOR APPLICATION NUMBER: 60/266,975
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 411
LENGTH: 855
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   YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patcurajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
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              CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
                                            APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids
FILE REFERENCE: 21402-258
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Padigaru, Muralidhara
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
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                                                                                                                         Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
                                                                                                                                                                      Colman, Steven D. Wolenc, Adam R. Pena, Carol E. A
                                                                                         Rieger, Daniel K.
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NUMBER: 60/265,102
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 418
LENGTH: 855
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Best Local
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APPLICATION NUMBER: 60/267,459
FILING DATE: 2001-02-08
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FILING DATE: 2001-02-07
APPLICATION NUMBER: 60/266,975
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FILING DATE: 2001-01-31
APPLICATION NUMBER: 60/266,406
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FILING DATE: 2001-01-31
APPLICATION NUMBER: 60/265,517
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 DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
                                                SQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
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                                 SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
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Best Local Similarity
Matches 851; Conserv
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APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: U$/10/600,187
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: U$/09/654,600A
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/421,213
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PRIOR FILING DATE: 1999-10-20
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                                                                   HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS
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Best Local Similarity
Matches 843; Conserv
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APPLICANT: Tang, Y. Tom et al
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Pol-
TITLE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF ESG ID NOS: 2700
SOFTWARE: Custom
SOFTWARE: Custom
SOFTWARE: Custom
SEQ ID NO 1798
LENGTH: 851
                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1798, Application US/10276774 Publication No. US20040053245A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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LVLLGIGFLVWHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKL
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Length

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186

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366 302 306

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Sequence 1143. Application US/10296115

Sequence 1143. Application US/2096115

Publication No. US20040053248A1

GENERAL INFORMATION:
APPLICANT: Hyseq Inc.
TITLE OF INVENTION: NO. US20040053248A1el Nucleic Aci
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/487,317
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1143
LENGTH: 851
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-296-115-1143
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   Sequence 1, Application US/10729807
Publication No. US20040132158A1
GENERAL INFORMATION:
APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer
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Best Local S
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                                                                                                             DWIKENTGV
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CURRENT FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US 09/889,238
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: PCT/US00/00641
PRIOR FILING DATE: 2000-01-11
PRIOR PPLICATION NUMBER: US 60/172,247
PRIOR APPLICATION NUMBER: US 60/172,247
PRIOR FILING DATE: 1999-01-11
PRIOR PRIOR DATE: 1999-01-11
PRIOR PPLICATION NUMBER: US 60/132,253
PRIOR APPLICATION NUMBER: US 60/136,653
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 39
PRIOR PPLICATION NUMBER: US 60/136,653
PRIOR PILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 39
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Best Local Sim
Matches 759;
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SEQ ID NO 1
LENGTH: 762
TYPE: PRT
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APPLICANT: BAUGHN, Mariah R., LU, Dyung Aina
TITLE OF INVENTION: HUMAN DEPTIDASES
FILE REFERENCE: PF-0651-1 DIV
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                                                                     ALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERR
                                                                                                                          CLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTROARVVGGTDADEGEWPWQVSLH
                                                                                                                                                CLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLH
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Pred. No. 3.6e-310;
0; Mismatches 3;
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US-10-097-340-312
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US-10-097-340-312
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CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR PILING DATE: 2001-03-14
PRIOR PPLICATION NUMBER: 60/325,149
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR PILING DATE: 2001/09/26
PRIOR PILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
                                                                                                                                                              Query Match
Best Local Similarity 90.5
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SOFTWARE: FAStSEQ for Windows Version
SEQ ID NO 312
LENGTH: 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/311,732
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                                     61 VLIGLILVILGIGFLVWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV
                                                          61 VLIGLLLVLLGIGFLVWHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKV
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Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
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Karen GLATT
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Robert C. BAST, Jr.
Karen LU
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Pred. No. 1.7e-309;
1; Mismatches 4;
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RESULT 25
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APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meer
APPLICANT: Shimkets, Richar
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      APPLICANT:
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Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
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APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
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PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
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PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
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; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 88.2%;
Matches 754; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
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      NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
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                                               PPNIDCTWNIEVPNNQHVKVSFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS
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Pred. No. 2e-304;
0; Mismatches 3;
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APPLICANT: Allen, Keith D
APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING SER
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING SER
TITLE OF INVENTION: PROTEASE GENE DISRUPTIONS
FILE REFERENCE: R-386
CURRENT FILING DATE: 2001-07-06
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/217,449
PRIOR APPLICATION NUMBER: US 60/223,170
PRIOR APPLICATION NUMBER: US 60/223,170
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 60/223,460
PRIOR APPLICATION NUMBER: US 60/223,460
PRIOR APPLICATION NUMBER: US 50/223,460
PRIOR APPLICATION NUMBER: US 50/223,460
PRIOR APPLICATION NUMBER: US 50/223,460
PRIOR PILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 855
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                                                                                                                                                                                                                        LENGTH: 855
TYPE: PRT
ORGANISM: Mus musculus
-09-900-751-2
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                                                                        VLIGLLLVLLGIGFLVWHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKV
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81.5%; Pred. No. 2e-288;
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APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Serhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Gangolli, Esha
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
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            Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
Li, Li
Gangolli, Bsha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
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APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding San
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
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PRIOR APPLICATION NUMBER: 60/265,412
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Matches 697; Conserv
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NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver.
SEQ ID NO 355
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OR FILLING DATE: 2001-01-31
OR APPLICATION NUMBER: 60/266,406
OR FILLING DATE: 2001-02-02
OR APPLICATION NUMBER: 60/266,767
OR FILLING DATE: 2001-02-05
OR FILLING DATE: 2001-02-07
OR FILLING DATE: 2001-02-07
OR FILLING DATE: 2001-02-07
OR APPLICATION NUMBER: 60/266,975
OR APPLICATION NUMBER: 60/266,975
OR FILLING DATE: 2001-02-07
OR FILLING DATE: 2001-02-07
OR FILLING DATE: 2001-02-07
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                     NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
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PPNINCTWNIKVPNNRNVKVRFKLFYLVDPNVPVGSCTKDYVEINGEKYCGERSQFVVSS
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NSSKITVHFHSDHSYTDTGFLAEYLSYDSNDPCPGMFMCKTGRCIRKELRCDGWADCPDY
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Rieger, Daniel K.
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81.5%; Pred. No. 2e-288;
tive 73; Mismatches 85;
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APPLICANT: Legley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICATION: Proteins and Nucleic Acids Enception of the Company of the Company of the Company Application Number: US/10/072,012
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
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APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
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APPLICATION NUMBER: 60/265,395
FILING DATE: 2001-01-31
APPLICATION NUMBER: 60/266,406
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Wolenc, Adam R.
Pena, Carol E. A
Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
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Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond
Gusev, Vladimir Y.
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Shimkets, Richard
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PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR PELICATION NUMBER: 60/267,057
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 413
LENGTH: 855
TYPE: PRT
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Best Local Similarity 81.5%;
Matches 697; Conservative
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661
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Pred. No. 2e-288;
73; Mismatches 85;
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; ORGANISM: Rattus US-10-072-012-356
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CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
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                                                                                                SOFTWARE: Pate
SOFTWARE: Pate
; SEQ ID NO 356
FORGTH: 855
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Query Match
Best Local Similarity
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APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
                                                                                                                                   Remaining Prior Application
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
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                                                                                  LENGTH: 85
TYPE: PRT
                                                                                                                                                                                        PRIOR FILING DATE: 2001-02-08
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                                                                                                                                                                                                                                                                     FILING DATE: 2001-02-05
APPLICATION NUMBER: 60/267,057
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/266,767 FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/265,395
FILING DATE: 2001-01-31
APPLICATION NUMBER: 60/266,406
FILING DATE: 2001-02-02
                                                                                                                                                                                                      APPLICATION NUMBER: 60/267,459
                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                       FILING DATE: 2001-02-07
APPLICATION NUMBER: 60/266,975
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
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Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
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Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond
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Zerhusen, Bryan
Patturajan, Meera
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Rieger, Daniel K.
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Padigaru, Muralidhara
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Sequence 414, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Seytuek, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
                                                                                                                                                                                                                              RESULT 30
US-10-072-012-414
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APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Miller, Charles E.
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APPLICANT: Gusev, Vadimir Y.
APPLICANT: Gusev, Vadimir Y.
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APPLICANT: Wolenc, Adam R.
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
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APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine S.
APPLICANT: Rieger, Daniel K.
APPLICANT: NUMBER: 5002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,514
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 414
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OR PRILING DATE: 2001-02-02
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APPLICATION NUMBER: 60/266,975
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tive 79; Mismatches 85;
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	PQQITPRWMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT 840 	AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGBIRVINQTTCENLL 780 :: :	DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720 : :	DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID 660 -	SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 600	SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK 540	NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH 480 :	PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS 420	YNLTFHSSONVLLITLITNTERRHPGFEATFFQLPRNSSCGGRLRKAQGTFNSPYYPGHY 360 	HARCQWVLRGDADSVLSLTFRSFDVAPCDGHDSDLVTVYDSLSPMEPHAVVRLCGTFSPS 300

Search completed: November 29, 2004, 08:49:57 Job time: 118.183 secs

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US-09-370-838-83

Sequence 83, Appl

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Searched: Scoring table: Title: Perfect score: OM protein - protein search, using sw model Sequence: Run on: Lesued Patents AA:*
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:* US=09=936-333-27. 4 €83 BLOSUM62 Gapop 10.0 , Gapext 0.5 November 29, 2004, 08:20:59; Search time 32.2432 Seconds (without alignments) 1758.570 Million cell updates/sec 478139 seqs, 66318000 residues MGSDRARKGGGGPKDFGAGL.....PGVYTRLPLFRDWIKENTGV 855 478139

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 39, A	equence 7,	tent No. 55	equence 2,	equence 2,	equence 12.	equence 5,	equence 21,	equence 8,	equence 2,	education v	equence 6,	equence 9,	tent No. 55	equence 2,	equence 2,	equence 2,	equence 2,	equence 2.	equence 3,	equence 3,	equence 11,	equence 11,	equence 1,	equence 1,	equence 1,	equence 12,	equence 1,	equence 3,	equence 1,	equence 1.	equence 1,	equence 1.	equence 1.	equence 54,	equence 7,	tent No. 52	equence 1,	equence 1,	equence 5,	equence 1.	equence 29	equence 1,	equence 6,	equence 1,	equence 1,	equence 1,	equence 83	equence 1,	equence 1,	tent No. 52	equence 19,	equence 2,	equence 13,	equence 3,	quence 62,	equence 83,	equence 82,					
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Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
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CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
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                                           SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
                                                                              SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
                                                                                             SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Pro
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CTP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/27,337
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1999-10-20
I PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
I NUMBER OF SEQ ID NOS: 98
SEQ ID NOS: 98
TYPE: PRT
CREATION.
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US-09-644-600-2
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Best Local
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Similarity 99.5%;
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                                                                                   HARCOWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS
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PRIOR APPLICATION NUMBER: 09/421,213
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 2
SEQ ID NO 3
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Patent No. 6649741

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CURRENT FILING DATE: 2000-09-01
                                                                                                                              Matches
                                                                                                                                                           Query Match
                                                                                                                                                                                          OTHER INFORMATION: TADG-15-09-654-600A-2
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                                                                                                                                           Score 4653; DB 4;
Pred. No. 0;
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Sequence 10, Application US/09644600

Patent No. 6451500

Patent No. 6451500

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

ITITLE OF INVENTION: TADG-15: An Extracellular Serine Pro
ITITLE OF INVENTION: TADG-15: An Extracellular Serine Pro
CURRENT APPLICATION NUMBER: US/09/644,600

CURRENT APPLICATION NUMBER: US/09/644,600

CURRENT FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR APPLICATION NUMBER: 09/27,337

PRIOR APPLICATION NUMBER: 09/027,337

PRIOR APPLICATION NUMBER: 09/027,337
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ORGANISM: Mus muscul
FEATURE:
OTHER INFORMATION: E
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Local Similarity 81.1%; Pred. No. 4.8e-269;
hes 684; Conservative 71; Mismatches 88;
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                                       PQQITPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
                                                              VEYSTVVRPICLPDATHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTCEDLM
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RESULT 5 US-09-654-600A-10

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Sequence 10, Application US/09654600A

Patent No. 6649741

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/654,600A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
1998-02-20
VUMBER OF SEQ ID NOS: 98
SEQ ID NO 10
LENGTH: 902
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
COTHER INFORMATION: Epithin
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                                          DCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLISPNWLVSAAHCYID
                                                                       SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
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APPLICANT: Madison, Edwin L.

APPLICANT: Semple, Joseph Edward
APPLICANT: Coombs, Gary Samuel
APPLICANT: Coombs, Gary Samuel
APPLICANT: Coombs, Gary Samuel
APPLICANT: Ong, Edgar O.
APPLICANT: Araldi, Gian Luca
TITLE OF INVENTION: Inhibitors of Serine Protease Activity of Matriptase or
TITLE OF INVENTION: MTMSI
FILE REFERENCE: Corvas 255/049
CURRENT APPLICATION NUMBER: US/09/657,986B
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                     RESULT 7
US-08-200-900A-2
; Sequence 2, Application US/08200900A
; Patent No. 5665566
; Patent No. 1NFORMATION:
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US-09-657-986B-2
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Patent No. 6797504
GENERAL INFORMATION:
APPLICANT: Madison, E
APPLICANT: Semple, G
APPLICANT: Coombs, G
APPLICANT: Reiner, J
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo Sapiens
APPLICANT:
TITLE OF INVENTION: CL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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99.2%;
                          CLONING OF ENTEROKINASE AND METHOD OF USE 38
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Pred. No. 9.2e-88;
0; Mismatches 2;
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Best Local Similarity
Matches 181; Conserv
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APPLICATION UNMBER: US/08/200,900A

FILING DATE: 23-FEB-194

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Melinert, Maureen C.

REGISTRATION NUMBER: 31,544

REFERENCE/DOCKET NUMBER: 31,544

REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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  KPGVYTRLPLFRDWIK 850
                                                                                                                                                                              DAGH--QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNG 546
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                                                                                                                                                                                                                           ELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTT
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                                                                                                                                CENLLPQ-QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRN 834
                                                                                                                                                                                                                                                                                                                                   HCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALL 715
                                                                                                                                                                                                                                                                                                                                                                                            QCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAA
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US-08-794-042-2
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Best Local Similarity 32.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 520:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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 545
                             601 DCD---
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                                                                                                                                                                                                      439 GFLAEYLS---YDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSDELNC----SC
                                                                                                                                                                                                                                                            391 GVPAGTCPKDYVEI-NGEKYCGERSQFV-----VTSNSNKITVRFHSDQSYTDT
                                                                                                                                                                                                                                                                                                                       333 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02140
                                                                                    KDDCGDGSDEASC-----PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 600
                                                                                                                                              DAGH -- QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNG
                                                                                                                                                                                                                                   A------DVVEIRDGE---GDDSLFLAVYTGPGPVNDVFSTTNRMTVLFITDNMLAKQ 404
                                                                                                                                                                                                                                                                                          ELP--TDCGGPHDLWEENTTFTSINFPNSYPNQAFCIWNLNAQKGKNIQLHFQEFDLENI 355
QCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAA
                                                                                                                 DSSGLVQFRIQS----IWHV----ACAEN-----WTTQISDDVC-----QLLG
                                                                                                                                                                           GFKANFTTGYGLGIPEPCKEDNFQCKDGECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTT 464
                                                     ---LGTGNSSVPTFSTGGGPYVNLNTAP-----NGSLILTPSQQC-----LEDSLILL
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                         CGLRSFTRQA--RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAA 655
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                                                                                                                                                                                                                                                                                                                                                   Score 700.5; DB 4; Length Pred. No. 7.2e-43; P1; Mismatches 187; Indels
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PCT-US94-00616-2
; Sequence 2, Application
; GENERAL INFORMATION:
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Best Local Similarity
Matches 181; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 798 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                          545
             656
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linear
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 GVPAGTCPKDYVEI-NGEKYCGERSQFV------VTSNSNKITVRFHSDQSYTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ELP--TDCGGPHDLWEPNTTFTSINFPNSYPNQAFCIWNLNAQKGKNIQLHFQEFDLENI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLBP
HCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAFGVQERRLKRIISHFFFNDFTFDYDIALL
                                                                                       QCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFLAEYLS---YDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSDELNC----SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-----DVVEIRDGE---GDDSLFLAVYTGPGPVNDVFSTTNRMTVLFITDNMLAKQ
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                                                                                                                                        DCD----CGLRSFTRQA--RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAA
                                                                                                                                                                                                                                                    KDDCGDGSDEASC-----PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
                                                                                                                                                                                                                                                                                                                                                             DAGH--QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNG
                                                                                                                                                                                                                                                                                                                                                                                                                     GFKANFTTGYGLGIPEPCKEDNFQCKDGECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTT
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                                                                                                                                                                                                                                                                                                            DSSGLVQFRIQS-----IWHV----ACAEN-----WTTQISDDVC-----QLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.0%; Score 700.5; DB 5; 32.6%; Pred. No. 7.2e-43; tive 91; Mismatches 187;
                                                                                                                                                                                                NGSLILTPSOOC-
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                                                                                                                                                                                                   ----LEDSLILL
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CURRENT APPLICATION NUMBER: US/09/734,675;
CURRENT FILING DATE: 2000-12-13;
NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0;
SEQ ID NO 4;
LENGTH: 407;
TYPE: PRT
; ORGANISM: Human
US-09-734-675-4
    GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
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US-09-734-675-4
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US-09-685-166A-895
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APPLICANT: WEBSTER, Maxion et al
TITLE OF INVENTION: ISOLATED HUM
TITLE OF INVENTION: NUCLEIC ACI
TITLE OF INVENTION: USES THEREO
FILE REFERENCE: CL000862
                                                                                                                                                                                      Sequence 895, Application Patent No. 6630305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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Patent No. 6365391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTRRSKTLGQSLRIVGGTEVEEGEWPWQASLQWDG-SHRCGATLINATWLVSAAHCFT- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPGVYARVPRFTEWIQ 794
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                                                                                                                                                                                                                                                                                                            GVYTRVTALRDWITSKTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                 PQ----QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKP 836
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                                                                                                                                                                                                                                                                                                                                                                                           PQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAGIVSWGDECAKPNKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.4%; Score 583; DB 3; Length 407;
45.9%; Pred. No. 1.2e-34;
tive 37; Mismatches 83; Indels
                                                                                                                                                                                                           US/09685166A
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APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C21

CURRENT APPLICATION NUMBER: US/09/685,166A

CURRENT FILING DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 895

LENGTH: 492
FILE REPERENCE: 02973 00015

CURRENT APPLICATION NUMBER: US/09/879,792

CURRENT FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/211,224

PRIOR FILING DATE: 2000-06-13

PRIOR APPLICATION NUMBER: US 60/283,353

PRIOR APPLICATION NUMBER: US 60/283,648

PRIOR APPLICATION NUMBER: US 60/283,648

PRIOR APPLICATION NUMBER: US 60/283,648

PRIOR FILING DATE: 2001-04-16
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                                                                                                                                                                                                                                                                    Sequence 14, Application Patent No. 6734006 GENERAL INFORMATION:
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Best Local
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APPLICANT: Gedrich, Richard
TITLE OF INVENTION: Regulation of Human Transmembrane
TITLE OF INVENTION: Protease
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Carter, Darrick
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Vedvick, Thomas
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Pred. No. 1.1e-32;
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US-09-879-792-14
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NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 895,
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Best Local Similarity 33.9%;
Matches 131; Conservative 5
SOFTWARE: F
SEQ ID NO 895
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                          APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ. ID NOS: 895
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TYPE: PRT
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                FastSEQ for Windows Version
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Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                            Robert A.
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APPLICANT: Teng, DAvid H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TENERSS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/342,749
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo s
US-09-679-426-895
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US-09-342-749-2
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Best Local
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                                                                                                                                     Matches
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Best Local Similarity
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                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                     LENGTH: 492
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                                                                                                                                                     Similarity
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PVCQDDWNENYGRAACRDMGYKNNFYSSQGIVDDSGSTSFMKLNTSAGNVDIYKKLYHSD
                                  GCSCPAQTFRC-SNGKCLSKSQQCNGKDDCGDGSDEASCPKV---NVV----
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                                                                  GSKCSNSGIECDSSGTCINPSNWCDGVSHCPGGEDENRCVRLYGPNFILQVYSSQRKSWH
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                                                                                                                                    Conservative
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                                                                                                                                    56;
                                                                                                                                  Score 555.5; DB 3
Pred. No. 1.6e-32;
6; Mismatches 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484
                                                                                                                                                                   DB 3;
                                                                                                                                     130;
                                                                                                                                     Indels
                                                                                                                                                                   Length 492;
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     229
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RESULT 15
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-691-840-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/342,749
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/091,044
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/691,840
CURRENT FILING DATE: 2000-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, DAvid H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
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401
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                                                                                                                                                                                                                                                                                                                                                                                                                                          522 GCSCPAQTFRC-SNGKCLSKSQQCNGKDDCGDGSDEASCPKV---NVV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSDEK-----DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLIS
                                                                                                                                                                                                                                                                               GSDEK-----DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLIS 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGPL--VTSKNNIWWLIGD
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                                                                           TKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEEKGKTSEVLNAA 400
                                                                                                                                                                                                                                                                                                                                                              TSWGSGCAKAYRPGVYGNVMVFTDWI 484
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                                                                                                                                                                                                  PNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS-QRSAPGVQERRLKRIISHPFFNDF 706
                                                                                                                                                                                                                                       ACSSKAVVSLRCIACGVNLNS-SRQSRIVGGESALPGAWPWQVSLH-VQNVHVCGGSIIT
  KVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGPL--VTSKNNIWWLIGD
                                     EIRVINQTTCEN--LLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFG-AGV
                                                                                                                    TFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKG
                                                                                                                                                          PEWIVTAAHCVEKP----LINNPWHWTAFAGILROSFMFYGAGYO---VEKVISHPNYDSK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 555.5; DB 4; 33.9%; Pred. No. 1.6e-32; tive 56; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 492;
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APPLICANT: COHER, MAUF
APPLICANT: COLFITTS, T
APPLICANT: FRIEDMAN, E
APPLICANT: GRANADOS, E
APPLICANT: KLASS, MICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 65,
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/235-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.

APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTIN

TITLE OF INVENTION: OF THE PROSTATE

NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Abbott
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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615 VVGGTDADBGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 TSWGSGCAKAYRPGVYGNVMVFTDWI
                                                    56 ILGLHMKSNLTSPQTVPRLIDEIVINPHYNRRRKDNDIAMMHLEFKVNYTDYIQPICLPE
                                                                                                                      1 IVGGSNAKEGAWPWVVGLY-YGGRLLCGASLVSSDWLVSAAHCVYG----RNLEPSKWTA
                                                                                   FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPD 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Abbott
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44.7%; Pred. No. 4.6e-32;
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                                                                                                                                                                                             Indels
                                                                                                                                                                                                                            Length 235;
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US-08-807-151-3
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBa:
CLONE: 416132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 31/2
STREET: 31/2
STRY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED TITLE OF INVENTION: PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CONCERNING SYSTEM: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J
REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: Filed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                                                                                                                                                                                                                             615 VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTA 674
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                                  794 LSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIK 850
                                                                                                                                                                      675 FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPD 734
                                                                                                    735 ASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQ-QITPRMMCVGF 793
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                                                                                                                                                                                                          1 IVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAAHCVYG----RNMEPSKWKA
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                                                                    ENQVFPPGRICSIAGWGALIYQGSTADVLQEADVPLLSNEKCQQQMPEYNITENMVCAGY 175
                                                                                                                                      VLGLHMASNLTSPQIETRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPE 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 amino acids
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Lal, Preeti
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DSCQGDSGGPLMCQE-NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWIQ 231
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RESULT 19
US-09-518-046-2
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US-09-478-957-3
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Patent No. 6350448
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                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL HU
TITLE OF INVENTION: PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/80
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7-
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ADDRESSEE: Incyte Pharmaceuticals,
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                                                                                                                                                                                                                                                                                                                                                                          Local
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
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CITY: Palo Alto
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                                                                                                       794 LSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIK 850
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Sequence 2, Application US/09518046

175

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Sequence 4, Application US/10177661

Patent No. 6794173

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Vicca, G. Duke

TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SER

FILE REFERENCE: 3256-A

CURRENT APPLICATION NUMBER: US/10/177,661

CURRENT FILING DATE: 2002-06-20

PRIOR APPLICATION NUMBER: US 60/299,606

PRIOR FILING DATE: 2001-06-20

NUMBER OF CO. T. NO. 1
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US-10-177-661-4
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SEQ ID NO 2
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity 33.6%;
Matches 128; Conservative 9
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GENERAL INFORMATION:
                                                                 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518,046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261,416
EARLIER FILING DATE: 1999-03-03
                                                                                    NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
ORGANISM: Homo sapiens
                      LENGTH: 446
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
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Pred. No. 3.5e-31;
52; Mismatches 130
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                                                                                                                                               Best Loc
Matches
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APPLICANT: Anderson, Dirk M.
APPLICANT: Virca, G. Duke
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10177661 Patent No. 6794173
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                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/177,661
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 60/299,606
PRIOR FILING DATE: 2001-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE FILE REFERENCE: 3256-A
                                                                                                                                                                                                                                PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(418)
OTHER INFORMATION: Xaa = unknown
                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Consensus sequence
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                          y Match 11.1%; Score 517.5; DB 4; Local Similarity 30.7%; Pred. No. 7.7e-30; hes 128; Conservative 43; Mismatches 161;
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62 NWNESYSXXACXQMGXXSAXYXSEXGXXXRXGANSFXKLNVSPXNLLXXDXYTSXIQXXL 121
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                                    GSDEA-----
                                                                      CIPXSXWCDGVXDCPXGEDEXXCVXXXXXGPXXXVRLYGDXXLLQVYSSSXXXWXPVCSD
                                                                                                           CKPLFWVCDSVNDCGDNSDEQGC----SCPAQTFRCSNGKCLSK---SQQCNGKDDCGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDC------DCGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433
                                      ----SCPKVNV-----
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RESULT 22
US-08-807-151-1
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   Best Local Similarity
Matches 111; Conserva
                                       Query Match
                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Bandman
APPLICANT: Lal, P
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
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CITY: Palo Alto
CTATE: CA
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 5
                                                                                                                              IMMEDIATE SOURCE:
                                                                             LIBRARY: SCORE: 556016
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                                                                                                                                                   TOPOLOGY:
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10.9%; Score 509.5; DB 3; 39.5%; Pred. No. 1.8e-29; tive 47; Mismatches 100;
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                                    Length 283;
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   Gaps
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                                   Matches
                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                            IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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APPLICATION NUMBER:
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TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
TITLE OF INVENTION: PROTEASE
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                                                                                                              LIBRARY: SUL
                                                                                                                                                                                            LENGTH: 283 amino acids
TYPE: amino acid
STRANDEDNESS: single
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581 SKGNPECDGKEDCSDGSDEK-----DCDCGLRSFTRQARVVGGTDADEGEWPWQVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        752 HTQYGGTGALILQKGEIRVINQTTCEN--LLPQQITPRMMCVGFLSGGVDSCQGDSGGPL
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                                      Conservative
                                                                                                                                             SCORNOT01
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                                                                                                                                                                               linear
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                                    10.9%; Score 509.5; DB 3; 39.5%; Pred. No. 1.8e-29; tive 47; Mismatches 100;
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                                      Indels
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                                      23;
                                      Gaps
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RESULT 24
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-661-2
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CURRENT APPLICATION NUMBER: US/10/177,661
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 60/299,606
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Patent No. 6794173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M.
APPLICANT: Virca, G. Duke
TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 10.9%; Score 509.5; DB 4; Local Similarity 32.3%; Pred. No. 3.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 -- VEKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWG
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411
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                         SGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWI 849
                                                                                                                                                                                                                                                               WPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDR----GFRYSDPTQWTAFLG---
                                                                                                                                                                                                                                                                                                                                          HTYRCLNGLCLSKGNPECDGKE----DCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGE 625
                                                                                                                                                                                                                                                                                                                                                                                S--NWNDSYSEKTC-------QLGFESAHRTTEVAHRDFANSFSILR
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                                                                                                                                                  LHQLPEAAS-----IAEIIINSNYTDEEDDYDIALMRLSKPLTLSAHIHPACLPMHGQ
                                                                                                                                                                                                                           WPWQVSLH-FGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEG------WKVYAGTSN
                                                                                                                                                                                                                                                                                                     YNSTIQESTHRS----ECPSQRYISLQCS------HCGLRAMT--GRIVGGALASDSK 246
RGGRDSCQGDSGGPL-VCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWI
                                                                       TFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDL
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CURRENT APPLICATION NUMBER: US/09/879,792

CURRENT FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/211,224

PRIOR FILING DATE: 2000-06-13

PRIOR APPLICATION NUMBER: US 60/283,353

PRIOR APPLICATION NUMBER: US 60/283,648

PRIOR APPLICATION NUMBER: US 60/283,648

PRIOR APPLICATION NUMBER: PCT

PRIOR APPLICATION NUMBER: PCT

PRIOR APPLICATION NUMBER: PCT

PRIOR APPLICATION NUMBER: PCT

PRIOR APPLICATION NUMBER: PCT
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NUMBER OF SEQ ID NOS: 36
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 12
LENGTH: 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.9%;
Best Local Similarity 32.3%;
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APPLICANT: Gedrich, Richard
TITLE OF INVENTION: Regulation
TITLE OF INVENTION: Protease
                                                                                    436
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                                                                                                                        VFPAGKAIWVTGWGHT-QYGGTGALILQKGEIRVINQTTCENLL--PQQITPRMMCVGFL 794
                                                                                                                                                                                                                                                              WPWQVSLH-FGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEG------WKYYAGTSN
                                                                                                                                                                                                                                                                                                                                                                                             HTYRCLNGLCLSKGNPECDGKE----DCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGE 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPKHAVRCDGVVDCKLKSDELGCVRFDWDKSLLKIYSGSSHQ------WLPICS
RGGRDSCQGDSGGPL-VCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWI
                             SGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWI
                                                                                      TFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 509.5; DB 4;
Pred. No. 4.3e-29;
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RESULT 26
US-08-508-448C-25
; Sequence 25, Application US/08508448C
; Patent NO. 5804410
; GENERAL INFORMATION:
; APPLICANT: KAZUYOSHI YAMAOKA et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

FOR PRODUCING THE

ENZYME

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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Secriet, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS (
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US)
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acid
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FILING DATE: July 28, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 3,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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CITY: Washington
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                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 NSGNLEINPSTEITSLTDQAAANWLINECGAGPDLITLSEQRILGGTEAEEGSWPWQVSL
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                                                                                                                                                                                                                                                                                                                                     L--VQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWIRQQTGI 418
                                                                                                                                                                                                                                                                                                                                                                     LSSVEADGR--IFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIKENTGV 855
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 83
LENGTH: 418
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 82
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APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roaddoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US
FILE REFERENCE: 210121.475C1
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
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TYPE: PRT
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                                                                        R-LNNAHHCGGSLINNMWILTAAHCFRSN----SNPRDWIATSGI----STTFPKLR-M
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GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 82
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-854-133-82
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US-09-854-133-82
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APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: CMPOSITIONS AND METHODS
TITLE OF INVENTION: THE THERAPY AND DIAGNOS
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
                                                                                                                                                                                                                           Sequence 83, Application US/09854133
Patent No. 6759508
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.9%; Score 508.5; DB 4; Best Local Similarity 37.4%; Pred. No. 3.5e-29; Matches 108; Conservative 52; Mismatches 100;
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; TYPE: PRT
; ORGANISM: Homo sapien
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 83
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                 LSSVEADGR--IFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIKENTGV 855
                                                                         QEYAGHTVPELRQGQVRIISNDVCN--APHSYNGAILSGMLCAGVPQGGVDACQGDSGGP
L--VQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWIRQQTGI
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Post-processing: Minimum Match 0%
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Adi16883 Human NOV
Adi1688676 Human NOV
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Aao29191 Human mem
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Result

Minimum Maximum

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The present sequence is that of the full-length form of human matriptase, a trypsin-like protease. This has an additional 172 amino acids compared with the truncated form of matriptase given in AAB19551. Either form can be produced in transformed or transfected cells using a claimed method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matriptase; serine protease; human; breast cancer; pre-malignancy; actinic keratosis; leukoplakia; Barrett's epithelium; columnar metaplasia; ulcerative colitis; bowenoid papulosis; adenomatous colorectal polyp; Qyerat erythroplasia; vulvar intraepithelial neoplasia; tumour; metastasis; therapy.
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                                             DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGH1CGASL1SPNWLVSAAHCYID
                                                                                                      SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
                                                                                                                                              SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
                                                                                                                                                                                                 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
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  DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
                              DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
                                                                                      SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
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                                                                                                                                                                                Sequence 855
                                                                                                                                                                                                                                                                                                               diagnosis, prognosis and
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KDALKILYSGVPFIGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM
                                                   VLIGLLLVLLGIGFLVWHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKV
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                                                                                human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (1g)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
                                                                                                                                                        Human NOVX protein homologue
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Li L, Gango
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Gangolli EA, Pad
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VL, Taupier RJ, Gusev VY,
K, Grosse WM, Alsobrook JP,
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VY, Colman SD,
JP, Lepley DM,
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son DW, Rastelli L, Miller
lman SD, Wolenc AR, Pena C
spley DM, Rieger DK, Burge
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                     SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
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thereof, which have properties related to the stimulation of biochemical complying properties related to the stimulation of biochemical complying properties in a cell, tissue, organ or organism. Complying the responses in a cell, tissue, organ or organism. Complying the responses in a cell, tissue, organ or organism. Complying the response of biologically active fragments for chiang notice and prognostic assays and furthermore in the treatment of complying the response of the treatment of the use of biologically active fragments for complying antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polymucleotides and antibodies are useful in the treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune completers, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, arthitis, Alzheimer's disease, infections, stroke, muscular dystrophy cand epilepsy. Accordingly, these molecules have many activities including cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antiastatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, cassays to identify small molecules that modulate or inhibit, for example, assays to identify small molecules that modulate or inhibit, for example, caff as in chromosome mapping, tissue typing, preventive medicine and coff the invention.

The invention.

SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVBINGEKYCGERSQFVVTS HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA MGSDRARKGGGGFXDFGAGLKYNSRHEKVNGLEEGVEFLFVNNVKKVEKHGPGRWVVLAA YNLTEHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTENSPYYPGHY MGSDRARKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA Score 4659; DB 5; Pred. No. 9.4e-308; 0; Mismatches 3; Length 855; Indels 0 Gaps 120 540 600 540 480 480 420 420 360 360 300 240 180 180 120 60

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12-PEB-2001
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17-PEB-2001
17-PEB-2001
17-PEB-2001
17-PEB-2001
11-PAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity, asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
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 2001US-0265412P

2001US-0265514P

2001US-0265914P

2001US-0266969

2001US-0266975P

2001US-0267959P

2001US-0267959P

2001US-0267959P

2001US-0271859P

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29-WAR-2001

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11-APR-2001

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20-APR-2001

23-APR-2001

03-WAY-2001

03-WAY-2001

03-WAY-2001

19-WAY-2001

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2001US-0294073P.
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2001US-0312020P.
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2001US-0312908P.
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2001US-03129115P.
2001US-0318115P.
2001US-0318115P.
2001US-03181115P.
2001US-03181115P.
2001US-031874P.
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Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Li L, Gangolli EA, Padigaru M, Anderson DW, Raste Gerlach VI, Taupier RJ, Gusev VY, Colman SD, Wolei Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rie ajan M, Shimkets RA; Rastelli L, Miller CE; , Wolenc AR, Pena CBA; M, Rieger DK, Burgess C G G

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing pharmacogenomics. 0 R

Disclosure; SEQ ID NO 419; 1498pp; English

Critis invention relates to a novel nucleic acids, and encoded polypeptides contereof, which have properties related to the stimulation of biochemical corphysiological responses in a cell, tissue, organ or organism. Critically, it refers to the use of biologically active fragments for cidiagnostic and prognostic assays and furthermore in the treatment of cidiverse pathological conditions. The present invention describes novel thuman and murine NOVX proteins, as well as methods to modulate their craments or preventing NOVX-associated disorders, e.g. cardiomyopathy, critically, respective, and peptide nucleic acids. Critically, conditions and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune critically, obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, canders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, canderstic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antiasthmatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, cassays to identify small molecules that modulate or inhibit, for example, caneurogenesis, wound healing and anoiocenesis. The nucleic arid are also consumers a wound healing and anoiocenesis. The nucleic arid are also consumers and anoiocenesis. neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.

Sequence 855 B

5.5 Score 4659; В ت. --Length 855;

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Matches 852; Conservative
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   protein homologue
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                                      entry)
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31-JAN-2001;
31-JAN-2001;
02-PEB-2001;
07-PEB-2001;
07-PEB-2001;
07-PEB-2001;
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15-PEB-2001;
16-PEB-2001;
11-MAR-2001;
11-MA
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     Zerhusen
   BD,
     Patturajan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 852
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VL, Taupier RJ, Gusev VY,
K, Grosse WM, Alsobrook JP,
                                                                                                                                                                                                  LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
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                             PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS
                                                                                                                                                                                                                                                                                                                                                                                                                 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM
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PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS
                                                                                                                                                 YNLTFHSSONVLLITLITNTERRHPGFEATFFOLPRMSSCGGRLRKAQGTFNSPYYPGHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 4659; DB 5;
Pred. No. 9.4e-308;
0; Mismatches 3;
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TY, Colman SD,
JP, Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rastelli L,
Wolenc AR,
M, Rieger DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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Pena CEA;
Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides
biochemical
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PR 21-N
PR 29-N
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PR 21-N
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13-NOV-2001;
21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
14-DEC-2001;
10-JAN-2002;
10-JAN-2002;
10-FEB-2002;
13-FEB-2002;
29-PAR-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; differential expression; cancer; angiogenic fibrotic disorder; psoriasis; ischaemia; heart dise
                                                                                                                                                                                                                                                                                                                                                              13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003042661-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease; autoimmune disease;
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2001US-0332464P

2001US-033539P

2001US-0340376P

2002US-0347211P

2002US-0347211P

2002US-0355250P

2002US-0355250P

2002US-0356714P

2002US-0358077P

2002US-0370110P

2002US-0370110P

2002US-0370246P
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SEQ ID disorder;

NO:C237

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

Whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a nucleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as sportasts, inchaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the presence or absence of a pathological cell in a useful for diagnosing, prognosing or treating cancer, comprises a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839F.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; SEQ ID NO C237; 1385pp; English.
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Murray
                                                                       PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS
                                                                                                                                                           YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
                                                                                                                                                                                                                                                  HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS
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                                                                                                                                                                                                                                                                                                                                        LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
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  NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
                                                                                                                                YNLTFHSSONVLLITLITNTERRHPGFEATFFOLPRMSSCGGRLRKAQGTFNSPYYPGHY
                                                                                                                                                                                                                     HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS
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R, Watson
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Pred. No. 9.
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Wilson
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E, Zlotnik
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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
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Bodary
Wu TD;
   Claim
                                         New PRO nucleic acid or polypeptide, useful pharmaceutical composition for diagnosing or
                                                                                        N-PSDB;
                                                                                                                                                                                                         25-SEP-2002; 2002US-0414006P
                                                                                                                                                                                                                                     25-SEP-2003; 2003WO-US030907.
                                                                                                                                                                                                                                                                   08-APR-2004
                                                                                                                                                                                                                                                                                                                                                        antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                   Antipsoriatic protein sequence
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DB; ADN04753.
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RESULT 8
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Best Local Simi
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 ADI16884;
                          ADI16884 standard; protein; 855
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                                                                                                                                                          PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
                                                                                                                                                                                                                                                                                                      DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
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nilarity 99.6%;
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Pred. No. 9.4e-308;
0; Mismatches 3;
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11-FEB-2001
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2001US-0265514P

2001US-0265514P

2001US-0265514P

2001US-0265517P

2001US-0266975P

2001US-0267823P

2001US-0267823P

2001US-0271835P

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2001US-0275947P

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2001US-028832P

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CC or physiological responses in a cell, tissue, organism or organism.

CC Specifically, it refers to the use of biologically active fragments for company or companism.

CC diagnostic and prognostic assays and furthermore in the treatment of conditions of the present invention describes novel to human and murine NOVX proteins, as well as methods to modulate their companism of the convention of the present invention describes novel companism or preventing NOVX-associated disorders, e.g. cardiomyopathy, contraining or preventing diseases such as inflammation, autoimmune contraining or preventing diseases inflections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antiasthmatic, nephrotropic, antiarthritic, hepatotropic, anorectic, converting muscularity, rirucide, antiparastic, converting manunosuppressive, antiparastic, converting manunosuppressive
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomics. of the invention.
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h VL, Taupier RJ,
K, Grosse WM, A
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                                                            YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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li EA, Pad
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99.5%;
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RJ, Gusev VY, Colman SD,
Alsobrook JP, Lepley DM,
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Rastelli L, Miller CE;
Wolenc AR, Pena CEA;
, Rieger DK, Burgess C
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11-APR-2001
11-AUG-2001
11-SEP-2001
11-SEP-2001
This invention relates to a novel nucleic acids, and encoded polypeptide thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and disbates. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrom
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Gerlach
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rosse WM, Alsobrook JP,
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VY, Colman SD, V
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son DW, Rastelli L, Miller CE;
Inan SD, Wolenc AR, Pena CEA;
epley DM, Rieger DK, Burgess C
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                      AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
                                                                 DRGFRYSDPTQWTVFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
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The present sequence represents a novel human extracellular serine protease, termed tumour antigen derived gene-15 proteain (see AAY06671), that is overexpressed in breast and overlan carcinomas. The TADG-15 gene (see AAX87815) can be used as a diagnostic and therapeutic target in ovarian carcinoma and other carcinomas including breast, prostate, lung and colon. The ligand binding domains of TADG-15 may be valuable in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel extracellular serine protease, termed tumor antigen-derived gene protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 855
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                                                                                               KDALKILYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                    VLIGLLLVLLGIGFLVMHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKV
                             YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLFRMSSCGGRLRKAQGTFNSPYYPGHY
  YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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larity 99.5%;
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15; extracellular serine
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                                                                    03-FEB-2000;
18-FEB-2000;
22-JUN-2000;
26-JUL-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transmembrane serine protease; membrane-type serine protease; MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatilung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therap
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2000US-0183542P.
2000US-0213124P.
2000US-0220970P.
2000US-00657986.
2000US-0234840P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to transmembrane serine proteases and their corresponding nucleotides and the protease domain of a type-II membrane-type serine protease (MTSP). MTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in gene therapy. The present sequence is human MTSP1 protein (also called matriptase)
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                      The invention relates to a purified single or two-chain polypeptide, which comprises the protease domain of a type-II membrane-type serine protease 7 (MTSP7) or its catalytically active portion. The polypeptide comprising MTSP7 is useful for detecting or diagnosing a neoplastic disease, a pre-malignant lesion, a malignancy or other pathologic condition in a subject. This polypeptide is also useful for monitoring tumour (e.g. tumour of the breast, cervix, prostate, lung, ovary or colon) progress and/or therapeutic effectiveness. The inhibitor of the polypeptide or treating or preventing a neoplastic disease, or tumour initiation, growth or progression, or a (pre-)malignant condition. The polypeptide or polynucleotide is also useful for identifying modulators of MTSP7, which may be used to treat cancers or tumours. This sequence represents a protein of the type-II membrane-type serine protease 1 relating to the
                                                                                                                                                                                                                                                                                     New transmembrane serine protease 7 (MTSP7) polypeptide for diagnosing neoplastic diseases, monitoring tumor progress or therapeutic effectiveness, or identifying MTSP7 modulators for treating tumors or
                                                                                                                                                                                                                                              Disclosure; Page 172-174; 184pp; English
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Pred. No. 2.4e-307;
D; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabe inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002;
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2001US-0265511P.
2001US-0265511P.
2001US-0266767P.
2001US-0266767P.
2001US-0267679P.
2001US-0267759P.
2001US-0267459P.
2001US-0271839P.
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2001US-02775947P.
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2001US-0275947P.
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infection; str.
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CC disgnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel CC human and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polynuclectides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC (AIDS), obesity, asthma, immunoslobulin (Ig)A nephropathy, cirrhosis, and epilepsy. Accordingly, these molecules have many activities including CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, cardiasthmatic, nephrotropic, antiarthritic, hepatotropic, antisatherial, virucide, antiparasitic, CC entiasthmatic, nephrotropic, antiatherial, virucide, antiparasitic, CC relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mappling, tissue typing, preventive medicine and CC of the invention. This polypeptide is a homologue of a human NOVX protein or the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel nucleic acids, and encoded polypeptid thereof, which have properties related to the stimulation of biochemica or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atherosclerosis, or diabetes,
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Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller
h VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE
K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
                                                                                                                                                                                                                                                                                                     LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
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                             YNLTFHSSONVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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Pred. No. 2.4e-307;
0; Mismatches 4;
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           This invention relates to a novel nucleic acids, and encoded polypeptide thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrom
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son DW, Rastelli L, Miller CE;
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epley DM, Rieger DK, Burgess C
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                                                               ABYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
                                                                                                      DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
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2001US-0265395

2001US-0265412P

2001US-0265517P

2001US-0266767P

2001US-0266767P

2001US-0267659P

2001US-0267859P

2001US-0267859P

2001US-0271839P

2001US-0271839P

2001US-0277848P

2001US-0275947P

2001US-0276450P

2001US-02764779P

2001US-0288327P

2001US-028834P

2001US-0288504P

2001US-0288504P

2001US-0294473P

2001US-0294904P
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VLIGLLLVLLGIGFLVWHLQYRDVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKV

VLIGLLLVLLGIGFLVWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV

MGSDRARKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA MGSDRARKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA

밁 5

Matches Query Match Best Local

851;

Conservative

Similarity

99.4%;

Score 4653; DE Pred. No. 2.4e. 0; Mismatches

4653; DB 5; No. 2.4e-307;

Length Indels

855;

0

Gaps

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121 121

180 120 120 60

61

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This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, alizates, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, CC artharitis, Alzheimer's disease, infections, stroke, muscular dystrophy CC antiarthy, accordiant, antiinflammatory, immunosuppressive, antiallergic, CC heemostatic, anti-IHIV, antidiabetic, antiarteriosclerotic, anorectic, antiartharic, heparterronic.
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16-AUG-2001;
21-AUG-2001;
28-AUG-2001;
31-AUG-2001;
07-SEP-2001;
19-SEP-2001;
19-SEP-2001;
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Gerlach
                                                       antiasthmatic, nephrotropic, antiarthritic, hepatotropic, neuroprotective, nootropic, antibacterial, virucide, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing
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Sequence
                                         pharmacogenomics. of the invention.
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18-OCT-2001;
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Gangolli EA, Padigaru M, Anderson DW, R
h VL, Taupier RJ, Gusev VY, Colman SD,
K, Grosse WM, Alsobrook JP, Lepley DM,
                                       invention
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2001US-0313390P.

2001US-0313390P.

2001US-0315470P.

2001US-0318147P.

2001US-0318118P.

2001US-0318118P.

2001US-0318740P.

2001US-0330379P.

2001US-0330308P.

2001US-0330308P.

2001US-0330301P.
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, Wolenc AR,
M, Rieger DK,
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Miller CE;
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RESULT 17
ABP56619
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AC ABP55
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DT 24-MJ
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DT Humar
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PN WO200
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PD 21-N0
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PR 14-MJ
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114-MJ
                                                                                                                                         type-II membrane-type matriptase.
                                                                                                                                                                     Human; membrane-type serine protease; enzyme; MTSP10; cytostatic;
                                                                                                                                                                                              Human membrane-type
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 14-MAY-2001; 2001US-0291001P
                            14-MAY-2002; 2002WO-US015332
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                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQPTCRTGRCIRKELRCDGWADCTDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
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                                                                                                                                                                                                                                                                                                                                                                                                               PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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                                                                                                                                                                                                serine
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                                                                                                                                                     serine protease; neoplastic
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The present invention describes a polypeptide comprising a purified comprise or two chain polypeptide, which comprises the protease domain of a C type-II membrane-type serine protease (MTSP10) or its catalytically cactive portion, or a matein of it, where up to 50 % of the amino acids c are replaced with another amino acid, and the resulting polypeptide is a c single chain or two chain polypeptide that has a catalytic activity of at C least 1-10 % of the unmutated polypeptide. MTSP10 has cytostatic c activity. The polypeptide containing the protease domain of the MTSP10 is useful for detecting a neoplastic disease, and for diagnosing the condition in a subject, or monitoring tumour (e.g. breast, cervix, c prostate, lung, ovary or colon tumour) progression and/or therapeutic c domain of MTSP10 is useful for treating or preventing neoplastic disease c in a mammal. An inhibitor of the polypeptide containing the protease in a mammal. An inhibitor of the polypeptide containing the protease c fithe MTSP10 polypeptide is useful for inhibiting tumour initiation, c growth or progression, or treating (pre-)malignant conditions of the e.g. C breast, cervix, prostate, lung, ovary or colon. The present sequence c represents human MTSP1 (also known as matriptase), which is used in an c c example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides comprising the protease domain of a type-II membrane-type serine protease (MTCP10), or its muteins, useful for diagnosing neoplasms or malignancies, or for screening for MTCP10 inhibitors for treating such diseases.
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Sequence A

Query Match Best Local

Local Similarity

99.4%;

Length 855;

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             NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
                                                                                    HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS
                                                                                                                                                                           LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
                                                                                                                                                                                         LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVBLMRFTTPGFPDSPYPA
NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
                                          PPNIDCTWNIEVPNNOHVKVSFKFFYLLEPGVPAGTCFKDYVEINGEKYCGERSQFVVTS
                                                    PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS
                                                                                                                                 HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPS
                                                                                                                                                                                                                      KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM
                                                                                                                                                                                                                                    KDALKILLYSGVPFIGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM
                                                                                                                                                                                                                                                                                                             MGSDRARKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA
                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 2.4e-307;
0; Mismatches 4;
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ARAGOLIT 18
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ID ARAGO
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The invention relates to serine protease 17 polypeptide designated CVSP17 and its corresponding nucleic acid sequence. The invention also relates to a method using CVSP17 protein to identify compounds that modulate its protease activity. The method is useful for preventing, diagnosing and treating disorders related to the serine protease 17 activity, such as
                                                                                                                                                                                                                                                   New substantially purified serine protease 17 polypeptide and encoding nucleic acid, useful for diagnosing and treating tumor conditions and/or cancer, particularly of the breast, cervix, prostate, lung, ovary or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease 17; CVSP17; tumour; breast; cervix; lung; ovary; colon; membrane-type serine protease; matri
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                                                                                  invention relates its corresponding
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DB; AAL60792.
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olon; gene therapy; human; enzyme; MTSP1;
matriptase.
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Matches 851
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                                          PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
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Matches 851; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to type II membrane-type serine protease 9 (MTSP9) polypeptides and polynucleotides. MTSP belongs to type II transmembrane serine protease (TTSP) family. Sequences of the invention and their antibodies are useful for diagnosing, treating or preventing neoplastic disease in mammals. They are useful for monitoring tumour progression, inhibiting tumour initiation, growth or progression or treating malignant or pre-malignant conditions. Transgenic animals of the invention are useful in animal models of tumour initiation, growth and/or progression models. The invention is also useful in gene therapy. The present sequence is human membrane-type serine protease 1 (MTSP1). MTSP1 also referred as matriptase is a member of the TTSP family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New substantially purified single or two-chain type II membrane-type serine protease 9 (MTSP9) polypeptide, useful for monitoring tumor progression, inhibiting tumor initiation, or treating a malignant or premalignant condition.
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15-MAY-2001; 2001US-0291501P.
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                                                                    DCDCGLRSFTROARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
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Query Match Best Local S Matches 851

Similarity

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                          The present sequence is the protein sequence of human type II transmembrane serine protease 1 (MTSP1). The invention relates to novel human type II transmembrane serine protein 20 (MTSP20) (see ABP72374) and nucleic acids encoding it (see ABZ58499). Also claimed are methods of inhibiting tumour initiation, growth or progression by inhibiting MTSP20 activity, and of treating or preventing a disease or disorder associated with undesired and/or uncontrolled angiogenesis or neovascularisation, especially undesired angiogenesis associated with solid neoplasms, vascular malformations and cardiovascular disorders, chronic inflammatory diseases, aberrant wound repairs, circulatory disorders, crest syndromes, dermatological disorders and ocular disorders using an inhibitor of MSP20
                                                                                                                                                                                                                                        New type-II membrane-type serine protease 20 polypeptides, useful for preparing a medicament for diagnosing, treating or preventing cancer, dermatological disorders, aberrant wound repairs or crest syndromes.
   Sequence
                                                                                                                                                                                                             Disclosure; Page 198-200; 216pp; English.
                                                                                                                                                                                                                                                                                                      N-PSDB;
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cytostatic; dermatological; cardiant; vulnerary; ophthalmological;
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Human; type I transmembrane serine protease 1; MTSP1; matriptase; serine protease; protease cleavage activation; diagnostic marker; neoplastic disorder; cancer; breast; cervix; prostate; lung; ovary; cytostatic; gene therapy; drug screening; tumour progression; monit enzyme.
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The invention relates to human type I transmembrane serine protease 25 (MTSP25; ADB97565) and polypeptides derived from it (e.g., ADB97555). The CC (MTSP25 gene is located on chromosome 12 MTSP25 is a serine protease CC which is activated by protease cleavage to yield a two-chain protease CC comprising an A chain and a B chain linked by a disulphide bond. MTSP25 (C comprising an A chain and a B chain linked by a disulphide bond. MTSP25 (C is expressed or is active in tumour cells, and can therefore be used as a CC diagnostic marker for certain cancers. The invention also encompasses (C nucleic acids encoding an MTSP25 polypeptide (ADB9754); nucleic acid vectors and host cells comprising an MTSP25 (C ADB9754); nucleic acid vectors and host cells comprising an MTSP25 (C EDB97554); nucleic acid vectors and host cells comprising an MTSP25 (C C ADB97554); nucleic acid vectors and host cells comprising an MTSP25 (C C Ether the single chain (zymogen) or two-chain (activated) form of C c either the single chain (zymogen) or two-chain (activated) form of C C treating neoplastic diseases, such as cancer of the breast, cervix, C C prostate, lung, ovary or colon. MTSP25 polypeptides may also be used for cidentifying compounds that modulate the protease activity of the c polypeptide and for monitoring tumour progression and/or therapeutic c effectiveness. The present sequence represents the related protein, MTSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified single- or two-chain polypeptide, useful for diagnosing, preventing or treating cancer (e.g. colon cancer), comprises a protease domain of a type-1 membrane-type serine protease 25 or its catalytically
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Sequence
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                                                                          LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
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       YNLTFHSSONVLLITLITNTERRHPGFEATFFOLPRMSSCGGRLRKAOGTFNSPYYPGHY
                                                                LPPRARSLKSFVVTSVVAPPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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Pred. No. 2.4e-307;
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 WPI; 20
                                                                                                                                                                                                       therapeutic agent; plasmin; protease specific antigen; PSA; cell-surface protease-associated disease; cancer; ocular disease; cardiovascular disease; chronic inflammatory disease; wound; circulatory disorder; dermatological disorder; rheumatoid arthritis; psoriasis; diabetic retinopathy; pterygium; excimer laser surgery scarring; glaucoma filtering surgery scarring; macular degeneration; crest syndrome; solid neoplasm; vascular tumou: melanoma; Kaposi's sarcoma; human; cell surface protease.
                                  Madison EL,
                                                                                    23-MAY-2001; 2001US-0293267P
                                                                                                           23-MAY-2002; 2002WO-US016819
                                                                                                                                    28-NOV-2002.
                                                                                                                                                                                                                                                                                                                   Human cell surface protease
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X444X8X2222222222222XXX Novel conjugate useful for treating cell-surface protease-associated disease, comprises a therapeutic agent and a peptidic or nucleic acis substrate linked to it optionally by a peptidic linker.

9; SEQ ID NO 2; 581pp; English

The invention comprises a conjugate that consists of a therapeutic agent and a peptide substrate (optionally linked via linker). The peptide substrate is proteolytically cleaved by a cell surface protease pr a soluble, released or shed form of it, to liberate the therapeutic agent, the conjugate of the invention is not substrantially cleaved by plasmin or protease specific antigen (PSA). The conjugate of the invention is useful for treating a cell-surface protease-associated disease such as: cancer, ocular diseases, cardiovascular diseases, chronic inflammatory diseases, wounds, circulatory disorders, dermatological disorders, rheumatoid arthritis, psoriasis, diabetic retinopathies, recurrence of pterygium, scarring from excimer laser surgery, scarring from glaucoma filtering surgery, macular degeneration, crest syndromes, solid neoplasms, vascular tumours, melanoma and Kaposi's sarcoma. The present amino acid sequence represents a human cell surface protease.

Sequence 855 A,

Query Match

Local

Similarity

99.4%;

Length 855;

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                                                                                                                                                                                                                                                                                           YNLTFHSSQNVLLITLI TNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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                                        DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
                                                                                         SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
                                                                                                                            SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
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 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
                        DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
                                                                          SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
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Pred. No. 2.4e-307;
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This sequence represents a human type II membrane-type serine protease 1 (MTSP1). The MTSP1 protein sequence was used in the isolation of the CC coding sequence of MTSP12, which has been isolated to chromosome 19. CC MTSP12 does not include the sequence of amino acids Arg-Lys-His-Leu-Pro-CC Arg-Pro-Ala ADG65347. The MTSP12 coding sequence was identified by using CC the protein sequence of the protease domain of MTSP1 to search the human CC HTGS database which produced three serine proteases of MTSP12-PD1, MTSP12-PD3. EST's were identified which matched portions of CC MTSP12-PD1, MTSP12-PD2 and MTSP12-PD3. MTSP12-PD3. MTSP12-PD3. EST's were identified which matched portions of CC cncers. These are useful in diagnostics, particularly for diagnosing CC cancers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. These are useful in immunoassays to detect, prognose, diagnose, CC concers. The prognose, diagnose, CC concers. The prognose in the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New type II membrane-type serine protease 12 proteins and nucleic acids, useful in diagnostics, particularly for diagnosing lung, esophageal, prostate, colon, ovary, cervix, breast and pancreas cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; type II membrane-type serine protease 12; MTSP12; chromosome 19; protease domain; MTSP12-PD1; MTSP12-PD2; MTSP12-PD3; lung; oesophageal; prostate; colon; ovary; cervix; breast; pancreas; cancer; tumour;
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                RLPLFRDWIKENTGV
                                                                PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
                                                                                                                     AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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                                                                                                      AEYSSMVRP1CLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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Pred. No. 2.4e-307;
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may be used
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                                                                                                                                                                                                                                                                   Sequence 855
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2; 205pp; English.
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                                                                               LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
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Pred. No. 2.
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ADJ46895 standard; (first protein; entry) ₽

Human transmembrane serine protease (MTSP) polypeptide

Human; transmembrane serine protease; MTSP; cell surface protease; plasmin; prostate specific antigen; PSA; prolliferative disease; plasmin; prostate specific antigen; PSA; prolliferative disease; concertifications disease; autoimmune disease; inflammatory disease; infectious disease; endocrine disease; cancer; ocular disorder; cardiovascular disorder; chronic inflammatory disease; wound; circulatory disorder; dermatological disorder; restenosis; rheumatoid arthritis; psoriasis; diabetic retinopathy; laser surgery scarring; glaucoma filtering surgery scarring; macular degeneration; CREST syndrome; bacterial infection; viral solid neoplasm; vascular tumour; lung; colon; prostate; melanoma Kaposi's sarcoma; viral disease;

sapiens

US2004001801-A1.

23-MAY-2002; 2002US-00156214

23-MAY-2002; 2002US-00156214

(CORV-) CORVAS INT

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CC The invention relates to a conjugate comprising a therapeutic agent and a CC peptidic substrate or nucleic acid substrate linked to the agent CC optionally through a linker or peptidic linker, where the peptidic CC substrate is proteolytically cleaved by a cell surface protease or a CC soluble, released or shed form conjugate to liberate the agent and the CC conjugate is not substantially cleaved by plasmin or prostate specific CC antigen (PSA). The conjugate is useful for treating a disease, which CC involves administering a conjugate to a subject, where the disease is CC preferably a proliferative diseases or a cell-surface protease-associated CC disease. The diseases include autoimmune diseases, inflammatory diseases, infectious diseases and endocrine diseases. The conjugate is useful for treating a conjugate comprising an agent and a peptidic substrate to confident and conjugate comprising an agent and a peptidic substrate to a subject exhibiting symptoms of a cell-surface protease-associated CC disorder, where the disease is selected from cancer, ocular disorders, cardiovascular disorders, chronic inflammatory diseases, wounds, CC circulatory disorders, dermatological disorders, restenosis, rheumatoid CC cardiovascular disorders, dermatological disorders, restenosis, rheumatoid CC cardiovascular toom glaucoma filtering surgery, macular degeneration, CC conjugate toom and Kaposi's sarcoma. This sequence represents a transmembrane CC serine protease (MTSP) polypeptide of the invention.
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Best Local S
Matches 851
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The invention relates to novel genes that are differentially expressed in sub-types of renal cell carcinomas and methods of detecting them using nucleic acids and probes. The nucleic acid probes hybridize with part or all of a coding sequence that is overexpressed in clear cell renal cell carcinoma (CC-RCC), papillary RCC, chromophobe/oncocytoma RCC,

Example IV;

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                                                                                                                                                                                                                        New nucleic acid and polypeptide compositions, useful in the field molecular biology and medicine, in particular for gene expression profiling, identifying diagnostic markers, and treating certain type
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neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antisanabylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; neurological disorder. Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

23-DEC-1999; 99US-00471275 21-JAN-2000; 2000US-00488725 25-APR-2000; 2000US-00552317 22-DEC-2000; 2000WO-US035017. 26-JUL-2001. (HYSE-) HYSEQ 2001-457603/49.)B; AAH99569. INC Drmanac

sapiens

Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

20; Page 237; 1217pp; English.

CC AAH99166 to AAH99904 encode the human proteins given in AAM2525 to CC AAW25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; CC entral nervous system; virucide; antiinflammatory; antirheumatic; CC candiovascular; antianaemic; antiaggregant; haemostatic; universary; CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides cencoding them can be used in gene therapy, antisense therapy and vaccine cytostation. The proteins and polynucleotides composits or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal contents, autoimmunity, genetic diseases, haematopoietic disorders, cardiac anaphylaxis, viral, bacterial, HIV and fungal contents, platelet disorders, thrombocytogaenia, wounds, burns, ulcers, CC antenna, platelet disorders, thrombocytogaenia, wounds, burns, ulcers, CC antenna, platelet disorders, thrombocytogaenia, wounds, burns, ulcers, CC antenna, diabetes, cancer, multiple sclerosis, depression, CC neuropathology, parkinson's disease, neurodegenerative and

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Pred. No. 1.1e-304;
1; Mismatches 5;
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haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin, chemotaxis; chemotinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; issue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiartlammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascutopic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human membrane-type Ser kinase homologue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine; cell proliferation; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor;
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09-AUG-2001

05-FEB-2001; 2001WO-US003800

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. (HYSE-) HYSEQ INC

ņ Drmanac

WPI; 2001-457740/49

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.

Claim 20; Page 188; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and convention also relates to vectors and recombinant host cells comprising a concludide of the invention, methods of producing the movel polypeptides, contibodies against the polypeptides, methods of identifying compounds which conditions the polypeptides, methods of identifying compounds which conditions are invention. Although novel, many of the cold bind to polypeptides of the invention have homology to known proteins, thereby conjupeptides of the invention have homology to known proteins, thereby conjupeptides of the invention have homology to known proteins, thereby conjupeptides of the invention have homology to known proteins, thereby contential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differential therapeutic applications. The polypeptides of the invention may commondulatory activity; activing the memoratic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be conditions are useful for preventing, treating or metastasis.

Conjuped in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic acids encoding them) may be used to promote wound cancers in the conditions in addition to immune disorders.

Conditions of burns, inclsions and ulcers), while those with commondulatory activities may be used in the treatment of viral, conditions in addition to immune disorders.

ABB11428

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Query Match
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Pred. No. 1.1e-304;
1; Mismatches 5;
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맑 8 В δ 밁 δ 밁 S

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Query Match
Best Local Similarity
Matches 798; Conserv

Conservative

91.9**%**; 95.8**%**;

Score 4302; DB 4; Pred. No. 1.9e-283; 7; Mismatches 24;

Length Indels

932;

Gaps

159 98

EKVNGLEEGVEELPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRV

QKVKNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAVTAF QKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRV 음 성 밁 Ş 뫄 δ 밁 δ 문 δ 멼 S 뫄 Ś 밁 δ 8 á 밁 ð 밁 ঠ

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ABG21142
ID ABG21142
ID AC ABG21
XX ABG21
XX 18-FE
XX 18-FE
XX Human
KW Human
KW Hood
OX Homo
OX Homo
XX Homo

                                                                                                                                                                                                                                                                                                          sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore mormal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity
                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
    Sequence 932 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 51801; 103pp; English
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23-AUG-2000; 2000US-00649167.
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BAC35125
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P98074 sus scrofa
Q72410 homo sapien
Q72411 homo sapien
Q72411 homo sapien
P98072 bos taurus
Q9y5q5 homo sapien
Q80yn4 rattus norv
Q8can9 mus musculu
P98073 homo sapien
P97435 mus musculu
Q9d319 mus musculu
Q9d319 mus musculu
Q9dg72 xenopus lae
Q6nuf5 xenopus lae
                                                                                                                                                                                                                                                                                       Q8iu80 homo sapien
Q6uxd8 homo sapien
Aaq88764 homo sapien
Q6icc2 homo sapien
Cag30332 homo sapi
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Q9dgr1 xenopus lae
Q8wc1 homo sapien
Q6wc1 homo sapien
Q6dev0 xenopus tro
Q6pf94 mus musculu
Aah57674 mus muscu
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Q8bik6 mus musculu
Bad18401 homo sapi
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Q9jji7 rattus norv
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Q9CS0
HATT HUMAN
TMS5_MOUSE
KALL RAT
PLAN PIG
Q6ZWK6
BACBS495
Q9EYE1
Q9EYE1
Q9EYE2
Q8CFE0
Q03711
Q7PWE4
Q96R84
Q8CC17
Q9PVY4
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AAHS1839
Q7ZT70
Q6GPF9
Q8BN10
Q6ZND6
BAD18439
Q81734
Q82NG3
AAQ88823
AAQ88823
AAQ88823
AAQ88823
AAQ88823
AAQ88823
BAD18806
Q8QXV0
Q9QZ74
Q8EQV5
Q8QXVI
Q9QZ74
Q8EQV5
Q8VIS1
TMS3_HUMAN
Q8VDVI
Q8VD
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Q91674
CCRAR_HUMAN
Q6IE15
Q6DUJ6
Q6DUJ6
Q96T73
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Q8CHN8
CRAR MOUSE
Q9Y1V3
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Q9JJS9
DES1_HUMAN
Q6UW31
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Q868H7
Q868H5
Q9XZM7
Q888H6
Q7TN04
Q920K3
TMS2 MOUSE
Q6P7D7
AAH61712
                          ALIGNMENTS
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09jjs9 rattus norv
09ul52 homo sapien
Aaq89376 homo sapien
Aaq89376 homo sapien
Aaq89376 homo sapien
Obchn8 rattus norv
P8064 mus musculu
09ylv3 polyandroca
07rty7 homo sapien
091674 xenopus lae
P48740 h complemen
06ie15 rattus norv
06duj6 cyprinus ca
096t73 homo sapien
015393 homo sapien
Aah51839 homo sapien
Aah51830 mus musculu
06znd6 homo sapien
Bad18439 homo sapien
Bad18439 homo sapien
                                                                              P06867 sus scrofa
Q6zwk6 homo sapien
Bac85495 homo sapien
Q9bye1 homo sapien
Q9bye2 homo sapien
Q9bye2 homo sapien
Q8cfe0 mus musculu
Q03711 xenopus lae
Q7pwe4 anopheles g
Q96r84 homo sapien
Q8cj17 rattus norv
Q9pvy4 xenopus lae
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061129 mus musculu
061129 gallus gall
Ass73179 gallus ga
09pu71 xenopus lae
09wuwa rattus norv
08cg43 rattus norv
08cg43 rattus norv
08cg43 mus musculu
092080 mus musculu
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O9gz74 rattus norv
O8rOp5 mus musculu
P26262 mus musculu
Q8jis1 triakis scy
P57727 homo sapien
O8vdvi mus musculu
Q8vhk8 mus musculu
Q7thx3 mus musculu
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Q6zmc3 homo sapien
Aaq88823 homo sapi
Bad18806 homo sapi
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Q9jiq8 mus musculu
Q6p7d7 rattus norv
Aah61712 rattus no
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Q7tn04
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AC 099576
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Blosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hitland D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whitling M., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Balterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Balterfield Y.S.N., Krzywinski M. Mayrs R.M.,

Balterfield Y.S.N., Krzywinski M. Mayrs M.,

Balterfield Y.S.N., Krzywinski M. Mayrs M.,

Balterfield Y.S.N., Krzywinski M. Mayrs M.,

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SEQUENCE FROM N.A.

MEDLINE=99432178; PubMed=10500122;

Takeuchi T., Shuman M.A., Craik C.S.;

Takeuchi T., Shuman M.A., Craik C.S.;

"Reverse biochemistry: use of macromolecular protease inhibitors to dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";

serine Acad. Sci. U.S.A. 96:11054-11061(1999).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last expense update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Merype serine protease 1) (MT-Sp1) (Prostamin) (Serine protease type serine prot
         Submitted [7]
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Cao J., F
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Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
"Molecular cloning of cDNA for matriptase, a matrix-degrading protease with trypsin-like activity.";
J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Blood, and Muscle;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1998)
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"Molecular cloning of a novel transmembrane serine protease expressed in human prostate.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               "Genomic
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                                               a novel human serine protease SNC19."; to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00431; CUB; 2.

R Pfam; PF00057; Ldl_recept a; 4.

R Pfam; PF00057; Ldl_recept a; 4.

R Pfam; PF00057; LDLRECEPTOR.

R PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00261; LDLRECEPTOR.

R PRINTS; SM00042; CUB; 2.

R SMART; SM000192; LDLB; 4.

R SMART; SM000192; LDLB; 4.

R PROSITE; PS01180; CUB; 2.

R PROSITE; PS01180; LDLRA 1; 2.

R PROSITE; PS01069; LDLRA 1; 2.

R PROSITE; PS01034; TRYPSIN_BLS; 1.

R PROSITE; PS010135; TRYPSIN_BLS; 1.

R PROSITE; PS010135; TRYPSIN_SER; 1.

R PROSITE; PS010135; TRYPSIN_SER; 1.

R PROSITE; PS010135; TRYPSIN_SER; 1.
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InterPro; IPR000859; CUB.
InterPro; IPR002177; LDL_receptor A.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
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                                                                                                                                                                                           Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:11344; ST14.
MIM; 606797; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and characterization of a complex containing matriptase and a Kunitz-type serine protease inhibitor from human milk.";
J. Biol. Chem. 274:18237-18242(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99303582; PubMed=10373425;
Lin C.Y., Anders J., Johnson M., Dickson R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION TISSUE=Milk;
                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity as defined by cleavage of synthetic substrates w or Lys as the P1 site.
SUBCELLULAR LOCATION: Type II membrane protein (Probable)
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 4 LDL-receptor class A domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005887; C:integral to plasma membrane; GO:0008236; F:serine-type peptidase activit
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protein (Potential).
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RLPLFRDWIKENTGV
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R -> V (in Ref. 3).
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Pred. No. 1e-313;
                                  CQGDSGGPLSSVEADGR I FQAGVVSWGDGCAQRNKPGVYT
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RESULT 2
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ID T16_OTT14 MOUSE
AC P56677;
DT 16_OTT2001
RM M.G. CI
RX MEDLINE=223885.7; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L.S., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Koeley R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Whiting M., Madan A., Schein J.E., Jones S.J.M., Marra M.A.,
RGeneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ",
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ",
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
C. - TSUBCELULIAR LOCATION: Type II membrane protein (Probable).
C. - SIMILARITY: Belongs to peptidase family Sl.
C. - SIMILARITY: Contains 2 CUB domains.
C. - SIMILARITY: Contains 2 CUB domains.
C. - SIMILARITY: Contains 2 CUB domains.
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STRAIN=C.B.17SCID; TISSUE=Thymus;

STRAIN=C.B.17SCID; TISSUE=Thymus;

MEDLINE=99216440; PubMed=10199918;

Kim M.G., Chen C., Lyu M.S., Cho E.G., Par

Schwartz R.H.;

"Cloning and chromosomal mapping of a gene

stromal cells encoding a new mouse type II

epithin, containing four LDL receptor modu

Immunogenetics 49:420-428(1999).
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
Suppressor of tumorigenicity 14 (EC 3.
Name=St14; Synonyms=Prss14;
Mus musculus (Mouse)
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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GO; GO:0009836; F:serine-type peptidase
GO; GO:0008236; F:serine-type peptidase
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR00903; Pept_Ser_Cys.
Pfam; PF000431; CUB; 2.
Pfam; PF00005; Ldl_recept_a; 4.
Pfam; PF00005; Ldl_recept_a; 4.
Pfam; PF00005; Ldl_recept_a; 4.
Pfam; PF00005; Ldl_recept_a; 4.
PFANTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00721; LDLa; 4.
SWART; SM00102; LDLa; 4.
SWART; SM00102; LDLa; 4.
SWART; SM00102; LDLa; 4.
SWART; SM00102; LDLa; 4.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; TRYPSIN_DOM; 1.
PROSITE; PS00068; LDLRA_7; 4.
PROSITE; PS000134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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Charge relay system (By Charge relay system (By N-linked (GlcNAC...)
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CUB 2.
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STRAIN=C57BL/6J; TISSUE=Kidney;
STRAIN=22354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The RIKEN Genome Exploration Research Grou
"Analysis of the mouse transcriptome based
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
Functional annotation of a full-length mo
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; R
NCBI TaxID=10090;
[1]
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14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
0 day neonate kidney CDNA, RIKEN full-length enriched l
clone:D630041B06 product: suppression of tumorigenicity
carcinoma), full insert sequence.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                  Nature
[3]
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REMBL, AKO52738; BAC35125.1; -. REMBL/GENBAN/16DD5 CRC64;
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; T
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Meth. Enzymol. 303:19-44(1999).
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PPNIDCTWNIEVPNNQHYKVRFKFFYLLBPGVPAGTCFKDYVEINGEKYCGERSQFVVTS
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                                                                                                       YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
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3; Mismatches 85;
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Q9JJI7;
       MEROPS; S01.302; -. GO; GO:000423; F:chymotrypsin activity; IIGO; GO:000823; F:peptidase activity; IEA. GO; GO:0004295; F:trypsin activity; IEA. GO; GO:0006508; P:proteclysis and peptidol; GO; GO:0006508; P:proteclysis and peptidol;
                                                                               SEQUENCE FROM N.A.

STRAIN-Wistar; TISSUE-Duodenum;
Inoue H., Takahashi K., Kishi K.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; AB037998; BAB03502.1; -.
EMBL; AB049189; BAB13765.1; -.
PIR; JC7731; JC7731.
HSSP; P00760; IEZX.
                                                                                                                                                                                                                                                         STRAIN=wistar; TISSUE-Jejunum;
MEDLINE=21498307; PubMed=11573963;
MEDLINE=21498307; PubMed=11573963;
Satomi S., Yamasaki Y., Tsuzuki S., Hitomi
"A role for membrane-type serine protease
                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Name=MBSP;
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Sciurognathi; Muridae; Murinae; Rat
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               peptidolysis;
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Best Local S
Matches 691
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InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001031; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PP00067; LdL_recept_a; 4.
Pfam; PP00067; LdL_recept_a; 4.
Pfam; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00721; LDLRECEPTOR.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CUB; 1; 2.
PROSITE; PS01209; LDLRA 1; 2.
PROSITE; PS00136; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 855 AA; 94955 MW; 35806B7ECF6CE
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Similarity 80.8%; Pred. No. 8e-259;
91; Conservative 79; Mismatches 8
DCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLISPNWLVSAAHCYID
                                                                                                                                                                               SQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
                                                                                                                                                                                                                                 SDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSK
                                                                                                                                                                                                                                                                                       NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQPTCRTGRCIRKELRCDGWADCTDH
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PPNINCTWNIKVPNNRNVKVRFKLFYLVDPNIFVGSCTKDYVEINGEKFCGERSQFVVSS
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                                                                                                                                                                 SOOCNGKDDCGDGSDEASCDNVNAVSCTKYTYRCONGLCLNKGNPECDGKKDCSDGSDEK
                                                                                                                                                                                                                                                                           NSSKITVHFHSDHSYTDTGFLAEYLSYDSNDPCPGMFMCKTGRCIRKDLRCDGWADCPDY
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                                                                                                                                                                                                                      SDERHCRONATHOFMCKNOFCKPLFWVCDSVNDCGDGSDEEGCSCPAGSFKCSNGKCLPQ
                                                                                                          FTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQD
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RC MEDLINE-22388257, PubMed=12477932;

RI MEDLINE-22388257, PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., McGernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Sodergran E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Bouffard G.G.,

RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Willalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergran E.D., Dickson M.C.,

RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences ";

RA Alteschide T. Warra M.A.,

RA Strauser T. S., Schmutz J., Mara M.A.,

RA Straus
                        InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR002172; LDL receptor S.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF000431; CUB; 2.
Pfam; PF00057; Ldl recept a; 4.
Pfam; PF00059; Trypsin; 1.
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05-JUL-2004
05-JUL-2004
Pfam; PF
Pfam; PF
PRINTS;
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MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; BC071077; AAH71077.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and initiative.";
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Name=st14-A-prov;
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Query Match
Best Local S
Matches 472
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SMART; SM00042; CUB; 2.
SMART; SM00042; CUB; 4.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLRA 1; 2.
PROSITE; PS50068; LDLRA 2; 4.
PROSITE; PS50068; LDLRA 2; 4.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 845 AA; 93593 MW; B917386C95BC
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                MMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRD
                                                            QVPDNKFVKVRFNMFYLAEPGVPVTKCTKDFVEIKGQKYCGEKEFFVVSNNSSKMSVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVRFH 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQN
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                                                                                                                          DASLWTAYLGLHDQAQLNTKDVVERKIKRIMAHIGFNDNTYDNDIAVLELEKFVEYTDFI
                                                                                                                                          DPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMV
                                                                                                                                                                                                        SFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYS
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                                                                                                                                                                                                                                                                                                              -LQFRCVNSKLCKPSYFICDGVNDCGDSSDELACKCPNNTFKCGNGKCIPDSQKCDRVDN
                                                                                                                                                                                                                                                                                                                                            GHOFTCKN-KFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDD
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PFTKKSRIVGGVNADTGEFPWQVSLHAKGNKHTCGASLVSPTMLISAAHCFQDDHQMRYS
                                                                                                                                                                                                                                                CGDGSDEAECDQVLTTACTEYTYKCKNNQCITKKNPECDGENDCSDGSDENAAKCNCGKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%; Score 2686; DB 2; 55.7%; Pred. No. 3.7e-177; tive 154; Mismatches 212;
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Best Local S
Matches 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO0127; LDL receptor A.
InterPro; IPRO01272; LDL receptor A.
InterPro; IPRO01254; Peptidase S1.
InterPro; IPRO01314; Peptidase S1A.
InterPro; IPRO01314; Peptidase S1A.
InterPro; IPRO01314; Peptidase S1A.
InterPro; IPRO0131; CUB; 2.
Pfam; PF00057; Ldl recept a; 4.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00721; LDLREGEPTOR.
SMART; SM00102; LDLa; 4.
SMART; SM00103; Tryp SPC; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLRA; 1; 2.
PROSITE; PS01209; LDLRA; 1.
PROSITE; PS0133; TRYPSIN_DOM; 1.
PROSITE; PS0133; TRYPSIN_SRR; 1.
PROSITE; PS00134; TRYPSIN_SRR; 1.
PROSITE; PS00135; TRYPSIN_SRR; 1.
PROSITE; PS00135; TRYPSIN_SRR; 1.
PROSITE; PS00135; TRYPSIN_SRR; 1.
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SEQUENCE FROM N.A.

MEDILINE=20363741; PubMed=10903452;
Yamada K., Takabatake T., Takeshima K.;
"Isolation and characterization of three no from Xenopus laevis.";
Gene 252:209-216(2000).

-1- SIMILARITY: Belongs to peptidase family EMBL; AB038498; BAB08218.1; -.

HSSP; P00760; 3BTH.
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Q9DGR1;
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=XMT-SP1;
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70; Conservative
FVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRG
                                                                                                                  LLVMHFAYRNKFVNKLYTGYLTIANTFFIDAYENSTTABFSDLSAKVIDTLQTVYNGNKD
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                                                                                      IAPYLOKCSISAFSEGGGNNVIGYYWSEFSVPAFREAAFEKAISELKLPSVNPROR----T
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                                                                                                                                                                                                                                                                                                                                                                                                                 56.8%; Score 2660; DB 2; 55.4%; Pred. No. 2.4e-175; tive 152; Mismatches 216;
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Q8WVC1;
01-MAR-2002 (
01-MAR-2002 (
01-MAR-2004 (
ST14 protein
Name=ST14;
MEDLINE-22386257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Primates;
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annotation updat
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-! SIMMILARITY: Belongs to peptidase family $1.

C: SIMMILARITY: Belongs to peptidase family $1.

C: GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsid activity; IEA.

InterPro; IPR0012172; LDL receptor A.

InterPro; IPR001254; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR00132; LDL receptor A.

Pfam; PP00089; Trypsin; 1.

PFANTS; PR00122; CHYMOTRYPSIN.

PRINTS; PR00122; CHYMOTRYPSIN.

PRINTS; PR00122; LDLA; 4.

REMART; SM00109; Tryps SPC; 1.

REMART; PS00130; Tryps SPC; 1.

REMART; PS00130; Tryps SPC; 1.

REMOSITE; PS00134; TRYPSIN JUKNOWN 1.

PROSITE; PS00134; TRYPSIN JUKNOWN 1.

PROSITE; PS00135; TRYPSIN SER; 1.

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Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQA
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                                                                                    LSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLFLFRFDWIKENT
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                                                      LSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENT
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X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Altachul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
X Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
X Hopkins R.F., Jordan H., Konaldo M.F., Casavant T.L., Scheetz T.E.,
X Stampleton M., Gares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Stampleton M., Galin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Robert S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
X Hilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Hilalon D.K., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
X Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
X Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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MEDLINE=22388257; PubMed=12477932;
CFT-minberg R.L., Feingold E.A., Gr
GTT-minberg R.L., Feingold E.A., Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JUL-2004) to the
EMBL; BC076994; AAH76994.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2004
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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SEQUENCE 663 AA; 73914 MW;
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                                                                                                                                                                                                                                                                                                                                                                   KDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLLGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUSUSMKYNNRPQSMNGFEEGVEFLPAANTKKVEKAGPKKKLAIFGVVIGAALLSLTIG
                                                                                                                                                              FVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRG
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DAGOMIRIKFKTFKMEKCKANAGDFVMVYDSLSPIBPRAQIRICGIYPPSYNLTFFSSSN
                                                   DADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQN
                                                                                                                    IAPYLOOCSISAFSEGSDNNVVGYYWSEFSVPAFREEAFEKAISE---LKLPTVNLRORA
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(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1965; DB 2;
Pred. No. 2.2e-127;
20; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 192;
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A., Schein J.E.,
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RX MEDLINE=22388.57; Pubmeda12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                      Q6PF94;
                                                                                                                                                                                                                                                                                                                                                                                                                     Q6PF94
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                            Impress protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGBIRVINQTTCENLLPQQITPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVPDNKFVKLRFNMFYLAEPGVPVTKCTKDFVEINGQKYCGERKFFVVSNNSSKMSVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMLVTLVTDNVGKFPGFLAEFSQFPKTSLCGGYIRDASGVFTSPYFPGHYPPKIECIWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNI
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Rodentia;
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27,
27,
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Last seq
Last ann
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Best Local
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GO; GO:0005886; C:plasma membrane; IDA.
InterPro; IPR0002172; LDL receptor A.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001037; Ldl recept a; 2.
Pfam; PP00089; Trypsin; 1.
PFAM; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR007261; LDLARCEPTOR.
SMART; SM001020; Tryp SPC; 1.
PROSITE; PS001020; TUPS; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01209; LDLRA 1; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R. Submitted (SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.;
"Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to peptidase
                                                             423
                                                                                           430
                                                                                                                           363
                                                                                                                                                                                          304
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455
                               490
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                                                                                                                                                                                        WHSYYDPFLLSVKSVAFQDCQVNLTLEGRL-DTQGFLRTPYYPSYYSPSTHCSWHLTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                  SEGSVIAYYWSEFSIPOHLVEEAERVMAEERVV--MLPPRARSLKSFVVTSVVAFPTDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A
                                                                                                                           LDYGLALWFDAYALRRQKYNRLCTQGQWMIQNRRLCGFRTLQPYAERIPMVASDGVTINF
                                                                                                                                                       NQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGER-----SQFVVTSNSNKITVRF
                                                                                                                                                                                                                                                      L-EWTRVDCRDR----VAMYDAAGPLEKRLITSVYGCSRQEPVMEVLASGSVMAVVWKKG
                                                                                                                                                                                                                                                                                      FRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLITN
                                                                                                                                                                                                                                                                                                                       GLVILEASVNDIVVLNSTLGCYRYSYVNPGQVLPLKGPDQQTTSCLWHLQGPEDLMIKVR
                                                                                                                                                                                                                                                                                                                                                                                   GEGPLTCFFWFILDIPEY-----QRLTLSPEVVRELLVDELLSNSSTLASYKTEYEVDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQVYSGSLRVLNRHFSQDLGRRESIAFRSESAKAQKMLQELVASTR-LGTYYNSSSVYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKVKNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAVTAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEAAEPEGKFKPFKNTKR-----KNRDYVRFTPLLLVLAALVSAGVMLWYFLGYKAEVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEGVE----FLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLLGIGFLVWH-LQYR-DVRV
                             AGHOFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC-SNGKCLSKSQQCNGKD
                                                                                           HSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCD
                                                                                                                                                                                                                      TERRHPGF----EATFFQLPRMS-SCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPN
                                                                                                                                                                                                                                                                                                                                                   --TVQRTQDNSCSFGLHARGVELMRFTTPG--FP-DSPYPAHARCQWALRGDADSVLSLT
                                                             TSQISLTGPGVQVYYSLYNQSDPCPGEFLCSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SEP-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
-NGLCVP---ACDGIKDCPNGLDERNCVCRAM-FQCQEDSTCISLPRVCDRQP
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502
                               548
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RESULT 10
AAH57674
ID AAH57674
AC AAH577
DT 02-MA
DT 02-M
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RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Klausner R.D., Collins F.S., Wagner L.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RX Hopkins R.F., Jordan H., Moore T., Max S., Carninci P., Prange C.,

RX Hopkins R.F., Jorden R.B., Bonaldo M.F., Casavent T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavent T.L., Scheetz T.E.,

RX Bring R.F., Jorden R.B., Bonaldo M.F., Casavent T.L., Scheetz T.E.,

RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RX Raha S.S., Moguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Moguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Moguellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RX Raha S.S., Moguellano N.A., Sodergran E.J., Lu X., Gibbs R.A.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RX Raha S.S., Moguellano N., Sodergran E.J., Lu X., Gibbs R.A.,

RX Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RX Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RX Ryminski M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Ryminski M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Ryminski M. J., Skalska U., Smailus D.E., Schein J.E.,
Matches
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH57674
AAH57674;
                                                                                                                       Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC057674; AAH57674.1; -. SEQUENCE 799 AA; 89557 MW; 16315A646A4D5288 CRC64;
                                                                                                                                                                                                                 Strausberg R.
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STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S
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                                                                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis
                                   Local
                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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Conservative
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Rodentia;
                                23.8%; Score 1114.5; DB 31.6%; Pred. No. 2.1e-68;
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27,
27,
   140;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                               99:16899-16903 (2002)
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
      Mismatches
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                                                             DB 2;
                                                                Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                            full-length
   90;
   Gaps
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RESULT TMS6 MM AC Q9 DT 10 DT 10 DT 10 DT 71 GN Na GN Na GN Ma OC Eu
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Mame=Imprss6; (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
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    Craniata; Vertebrata; I
Sciurognathi; Muridae;
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    Euteleostomi; ; Murinae; Mus
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RC STRAIN—ECSTBL/GJ; TISSUE-Liver;
RC STRAIN=CSTBL/GJ; TISSUE-Liver;
RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Satto R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Satto R., Nogami A., Schombach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Balke J.A., Enadt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Schrimil L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schrimil L.M., Kanapin T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavana W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Ponttus J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wanner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Wilming L., Scholan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Hara A., Sakai K., Sawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Mineys E., Hayashizaki Y.,
RA Hara H., Scholan M., Waterston R., Lander E.S., Rogers J.,
REL Mature E., Hayashizaki Y.,
REL M., Scholan M., Waterston R., Lander E.S., Rogers J.,
REL M., Scholan M., Waterston R., Lander E.S., Rogers J.,
REL M., Scholan M., Waterston R., Lander E.S., Rogers J.,
REL M., Scholan M., Scholan M., Scholan 
MEDLINE=22668120; PubMed=12784999; Netzel-Arnett S., Hooper J.D., Sza Bugge T.H., Antalis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mouse matriptase-2: identification, characterization and comparative mRNA expression analysis with mouse hepsin in adult and embryonic
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                                                                                   cDNA sequences.";
l. Acad. Sci. U.S.A.
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                                                                                      99:16899-16903
                   Szabo
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                   Madison
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                   E.L.,
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EMBL; AY240929; AAP69827.1; -...
EMBL; AK004939; BAB23684.2; -...
EMBL; BC029645; AAP29645.2; -...
HSSP; P00760; IEZX.

MEROPS; S01.308; -...
MGD; MGI:1919003; Tmprs86.
G0; G0:0016021; C:integral to membrane; IDA,
G0; G0:0004252; F:serine-type endopept;
G0; G0:0001525; P:angiogenesis; ISS.
G0; G0:0004727; P:intracellular matrix
G0; G0:0047730; P:fibrinolysis; ISS.
G0; G0:0047730; P:fibrinolysis; ISS.
G0; G0:0047730; P:fibrinolysis and pepti
InterPro; IPR000859; CUB.
InterPro; IPR0012172; LDL_receptor A.
InterPro; IPR0012174; Peptidase_S1A.
InterPro; IPR0012174; Peptidase_S1A.
InterPro; IPR001374; Peptidase_S1A.
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GO; GO:0007243; P:intracellular signaling cascade; ISS.
GO; GO:0007243; P:intracellular signaling cascade; ISS.
GO; GO:0005508; P:proteolysis and peptidolysis; ISS.
                                                                                                                                                                                                                                                                                Pfam; PF00057; Ldl_recept_a; 2.

Pfam; PF00089; Trypsin; 1.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR007261; LDLRECEPTOR.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS50068; LDLRA 2; 3.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS50134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: Expressed at higher levels from 15.5 dpc with a peak at 13.5 dpc. Expression in the d liver as well as a restricted set of embrionic epithe the nasal cavity and pharyngo-tympanic tubes. SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 CUB domains. SIMILARITY: Contains 3 LDL-receptor class A domains.
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FUNCTION: May play a specialized role in matrix remodeling processes in liver (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: Expressed at highest levels in liver, kidn
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                                                                                                                                LCAGYRKGKKDACOGDSGGPLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYTRVTRVINW
                                                                                                                                                MCVGFLSGGVDSCQGDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDW
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); Mismatches
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Pred. No. 2.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
P -> PP (in Ref. 2).
; 32EB3E7C3127801B CRC64;
     PRT;
     811
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.1e-68;
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514 608 572 568 668 429 434 489 466 374

259 260 145

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RA Bagguley C., Balley M., Barlow K.F., Bates K.N., Beasley O.P.,
RA blird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burges J.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Davson B.,
RA Clegg S.M., Cockee C., Doddworth S.J., Durbin R.M., Ellington A.G.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Levershaw M., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mchammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA Mallians S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Williams S., Kawasaki K., Sasaki T., Asakaw S., Kudoh J.,
RA Williams S., Kawasaki K., Sasaki T., Asakaw S., Kudoh J.,
RA Wincahi A., Shibuya K., Yoshizaki Y., Aoki N., Wilney T.E., Wilming L.,
Wilning S., Lin S.-P., Loh P., Malaj E., Wguyen T., Pan H.,
RA Mang Q., Wang Y., Wang Z., White J., Benton S., Lai H., Lao H.I.,
RA Mang Q., Wang Y., Wang Z., White J., Benton S., Do A., Do T.,
RA Mang Q., Wang Y., Wang Z., White J., Wallingham D., Wu H., Yao Z.,
RA Mang Q., Chissoe S., Murray J., Miller N., Minx P.,
RA Cordes M., Du Z., Felton L., Geola D., Graves T., Hawkins J.,
RA Cordes M., Du Z., Felton L., Geola D., Graves T., Hawkins J.,
RA Cordes M., Du Z., Felton L., Shinson A., Wong A.C.C., Morrow B.E.,
RA Cordes M., Du Z., Shizuya H., Simon M.I., Dumanski J.P.,
RA Hunt S., Shizuya H., Simon M.I., Dumanski J.P.,
RA Cordes M., Du Z., Shizuya H., Simon M.I., Dumanski J.P.,
RA Cordes M., Du Z., Shizuya H., Simon M.I., Tapia I., Brader C.E.,
RA Cordes M., Wang A.C., M
MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peyrard M., Kedra D., Seroussi E., Franson. ... O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Khan A.S., Lane L., Tilahun Y., Wright H.; Khan A.S., Lane L., Tilahun Y., Wright H.;
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, East annotation update)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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NA sequence of human
402:489-495(1999).
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to the EMBL/GenBa
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .E., Bruskiewich R., Beare D.M.,
R., Almeida J.P., Babbage A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease."
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       , Scheetz T.E.,
, Prange C.,
, Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I., Bruder C.
Hu X.,
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Genew; HGNC:16517; TMPRSS6.
InterPro; IPR000859; CUB.
InterPro; IPR0002172; LDL receptor A.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.

P00760

PF00431; CUB; 1. PF00057; Ldl_recept_a; 2. PF00089; Trypsin; 1.

Pept_Ser_Cys.

PR00722; CHYMOTRYPSIN PR00261; LDLRECEPTOR.

SM00192; SM00020;

; LDLa; 3. ; Tryp_SPc; 1. 80; CUB; 1. CUB; 1.

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratn Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hu Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A. Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sa Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G. Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-le
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Petal liver;
MEDLINE=22241917; PubMed=12149247; DOI=10.1074/jbc.M203007200;
MEDLINE=22241917; PubMed=12149247; DOI=10.1074/jbc.M203007200;
Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.;
"Matriptase-2, a membrane-bound mosaic serine proteinase predominantly expressed in human liver and showing degrading activity against expressed in human liver and showing degrading activity against extracellular matrix proteins.",

2. Biol. Chem. 277:37637-37646(2002).
                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer Metastasis Rev. 22:237-258(2003)
-!- FUNCTION: May play a specialized ro
processes in liver.
-!- SUBCELLULAR LOCATION: Type II membr
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVIEW
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surface proteolytic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bugge T.H., Antalis
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                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q8IU80-2; Sequence=VSP_008379, VSP_008380;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Liver specific.
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 3 LDL-receptor class A domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences.";
                                               AJ319876;
AY055383;
AY055384;
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                                                                              CAC85953.1; ALT_INIT.
AAL16413.1; -.
AAH39082.1;
                                                  AAL16414.1;
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                   ANNOTATED CDS
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                                                                                                                                                                                      http://www.isb-sib.ch/announce/
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Gibbs R.A.,
igues S
                                                                                                                                                                                                                                                                                                                                                                                  domains.
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SEQUENCE
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                                                                                                                                                                                                                                                                  PS01209; LDLRA_1; 1.
PS50068; LDLRA_2; 3.
PS50240; TRYPSIN DOM; 1.
PS00134; TRYPSIN_HIS; 1.
PS00135; TRYPSIN_ER; 1.
                                                                                                                                   GQGQVLRLKGPDHLASSCLWHLQGPKDLMLKLRL-EWTLAECRDR----LAMYDVAGPLE
                                                                                                                                                                                                                                                                                                                                    GGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLL
KYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAG---ITINFTSQISLTGPGVRVH
                      VPAGTCPKDYVEINGEKYCG-----ERSQFVVTSNSNKITVRFHSDQSYTDTGFLAE
                                                               FQLPRMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPG
                                                                                        KRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSYYDPFVLSV-
                                                                                                             PHALVQL--CGTYPPSYNLT----
                                                                                                                                                                            QALLVEELLSTVNSSAAVPYRAE----YEVDPEGLVILEASVKDIAALNSTLGCYRYSYV
                                                                                                                                                                                                  KSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRF-----TTPGFPDSPY-
                                                                                                                                                                                                                        TSTR-LGTYYNSSSVYSFGEGPLTCFFWFILQIPEH
                                                                                                                                                                                                                                             SGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVMLPPRARSL
                                                                                                                                                                                                                                                                                                               GGQGDGGDG-----EEAEPEGMFKACE-----DSKRKARGYLRLVPLFVLL--ALLVLA
                                            FQACEVNLTLDNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLALWFDAYALRRQ
                                                                                                                                                                                                                                                                                                                                                                                                     116
811 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      462
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                      PAH--ARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPME
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SCHORT OF YAFTLSSIMIPPLEPEPSIPSTYTP GLYNQSDPCPGE -> YHFLSSIMIPPLEPPPSIPSSTYTP SLEAQUPNLRGAARGASRGWCQACCP (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136;
                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in 180.0.)
/FTId=VSP 008380.
A -> V (in Ref. 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
Signal-anchor for type II m
protein (Potential).
Extracellular (Potential).
CUB 1.
CUB 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine proteas
Charge relay s
Charge relay s
Charge relay s
                                                                                                                                                                                                                                                                                                                                                                     Score 1114; DB 1;
Pred. No. 2.3e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDL-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP 008379.
Missing (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                      7EEF193F655DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                             -----FHSSQNVLLITLITNTERRHPGFEATF
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                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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class
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m (By similarity).
m (By similarity).
.) (Potential).
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InterPro; IPRO00859; CUB.
InterPro; IPRO02172; LDL receptor A.
InterPro; IPRO01254; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1A.
InterPro; IPRO01314; Peptidase_S1A.
InterPro; IPRO09003; Pept_Ser_Cys.
Pfam; PF00431; CUB; 1.
Pfam; PF000431; CUB; 1.
Pfam; PF00089; Trypsin; 1.
PF100189; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLAECEPTOR.
SMART; SM00192; TDLAE; 3.
SMART; SM00192; TTYP_SPC; 1.
PROSITE; PS01180; CUB; 1.
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05-JUL-2004
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                               effort to identify novel human secreted bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to peptidase EMBL; AY358398; AAQ88764.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=22887296; PubMed=12975309;
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ORFNames=UNQ354;
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EGEWPWQASLQVRGR-HICGGALIADRWVITAAHCFQED---
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Primates;
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PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PSS0240; TRYPSIN_HIS; UNKNOWN_PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 802 AA; 88845 MM; 8726C91E
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                                                                                                                                                                                                                                                                NVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDAD
                                                                                                                       LFWVCDSVNDCGDNSDEQGCSCPAQTFRC-SNGKCLSKSQQCNGKDDCGDGSDEASCPKV 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QALLVEELLSTVNSSAAVPYRAE----YEVDPEGLVILEASVKDIAALNSTLGCYRYSYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVMLPPRARSL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGFLVWH-LQYR-DVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGQGDGGDG-----EEAEPEGMFKACE-----DSKRKARGYLRLVPLFVLL--ALLVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLL
                                                          LHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKGKKDACQ
                                                                               KAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQ
                                                                                                                                                                                                             EGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS
                                                                                                                                                                                                                                                                                                               ---ACDGVKDCPNGLDERNCVCRA-TFQCKEDSTCISLPKVCDGQPDCLNGSDEEQCQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                           KYDLPCTQGQWTiQNRRLCGLRILQPYAERIPVVATAG---ITINFTSQISLTGPGVRVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSYYDPFVLSV-----QPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGQVLRLKGPDHLASSCLWHLQGPKDLMLKLRL-EWTLAECRDR----LAMYDVAGPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRF-----TTPGFPDSPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAGVILWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELI
GDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQ 799
                                                                                                                                                                                     EGEWPWQASLQVRGR-HICGGALIADRWVITAAHCFQED---SMASTVLWTVFLGKVWQN
                                                                                                                                                                                                                                                                                                                                                                                                          YLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPAGTCPKDYVEINGEKYCG-----ERSQFVVTSNSNKITVRFHSDQSYTDTGFLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQLPRMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRPKFFYLLEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSTR-LGTYYNSSSVYSFGEGPLTCFFWFILQIPEH------RRLMLSPEV--V
                           GDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIKE 851
                                                                                                                                                                                                                                                  -GVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCDCGLQG--PSSRIVGGAVSS
                                                                                                                                                                                                                                                                                                                                                                             YGLYNQSDPCPGEFLCSV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQACEVNLTLDNRLDSQGVLSTFYFFSYYSFQTHCSWHLTVFSLDYGLALWFDAYALRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHALVQL--CGTYPPSYNLT------FHSSQNVLLITLITNTERRHPGFEATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PAH--ARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPME 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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88845 MW; 8726C91B1E02E163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 1112; DB 2; Length 8: 31.0%; Pred. No. 3.1e-68; tive 135; Mismatches 330; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                                                                                                                                                                                                                                                                                                                             ----NGLCVP
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Best Local Similarity
Matches 276; Conserv
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02-MAR-2004
02-MAR-2004
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AAQ88764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bioinformatics Assessment. ";
Genome Res. 13:2265-2270 (2003).
EMBL; AY358398; AAQ887641; -.
SEQUENCE 802 AA; 88845 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. PubMed=12975309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIGFLVWH-LQYR-DVRVQKVKNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLY
LFWVCDSVNDCGDNSDEQGCSCPAQTFRC-SNGKCLSKSQQCNGKDDCGDGSDEASCPKV
                                                                                                                                                                                                                      KRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSYYDPFVLSV------QPVV
                                                                                                                                                                                                                                                                                   GQGQVLRLKGPDHLASSCLWHLQGPKDLMLKLRL-EWTLAECRDR----LAMYDVAGPLE
                                                                                                                                                                                                                                                                                                                                                  QALLVEELLSTVNSSAAVPYRAE----YEVDPEGLVILEASVKDIAALNSTLGCYRYSYV
                                                                                                                                                                                                                                                                                                                                                                                 KSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRF-----TTPGFPDSPY-
                                                                                                                                                                                                                                                                                                                                                                                                                 TSTR-LGTYYNSSSVYSFGEGPLTCFFWFILQIPEH------RRLMLSPEV--V
                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMABERVVMLPPRARSL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGQGDGGDG----EEAEPEGMFKACE-----DSKRKARGYLRLVPLFVLL--ALLVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLL
                                                                                              KYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAG---ITINFTSQISLTGPGVRVH
                                                                                                                           VPAGTCPKDYVBINGEKYCG-----
                                                                                                                                                                                                                                                      PHALVQL--CGTYPPSYNLT------FHSSQNVLLITLITNTERRHPGFEATF
                                 YGLYNQSDPCPGEFLCSV---
                                                              YLSYDSSDPCPGOFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKP
                                                                                                                                                           FQACEVNLTLDNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLALWFDAYALRRQ
                                                                                                                                                                                       FQLPRMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPG
                                                                                                                                                                                                                                                                                                                    -----PAH--ARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Primata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.7%; Score 1112;
31.0%; Pred. No. 3
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8726C91B1E02E163 CRC64;
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                                                                                                                          ERSOFVVTSNSNKITVRFHSDQSYTDTGFLAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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                                  -NGLCVP
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RESULT 15
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Q6ICC2
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                                                                            Query Match
Best Local Simi
Matches 276;
                                                                                                                                                                        Pfam; PF00431; CUB; 1...

Pfam; PF00089; Ldl recept a; 2.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00726; LDLa; 3.

SMART; SM00192; Tryp SPC; 1.

SMART; SM00192; Tryp SPC; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01209; LDLaA 1; 1.

PROSITE; PS01209; LDLAA 2; 3.

PROSITE; PS0134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
DJ1170K4.2 protein.
Name=dJ1170K4.2;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6ICC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR001274; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR009003; Pept Ser Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Beare D.M., Dunham I.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Collins J.E., Wright C.L., Edwards C.A., Davis
Collins J.E., Wright C.L., Edwards C.A., Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- SIMILARITY: Belongs to peptidase EMBL; CR456446; CAG30332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                SEQUENCE
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      11
                                                                                                   Similarity
                                     GGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAAVLIGLLLVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDSGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCDCGLQG--PSSRIVGGAVSS
                                                                                                                                                              824 AA;
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                              91333 MW; A74F186406041F7B
                                                                            23.3%; Score 1092; | 30.3%; Pred. No. 7.8 | tive 135; Mismatches
    --EEAEPEGMFKACE-----DSKRKARGYLRLVPLFVLL--ALLVLA
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on update)
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Mokrab
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                                                                                 Indels
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Y., Huck
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01-JUN-2004 (TrEMBLrel. 2
01-JUN-2004 (TrEMBLrel. 2
DJ1170K4.2 protein.
                    Homo sapiens (Human)
                                           DJ1170K4.2.
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                                                                                                                                                                                                                                                                                                     RLPLFRDWIKE
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                                                                                                                                                              PRELIMINARY;
    Chordata;
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Last sequence update)
Last annotation updat
    Craniata;
                                                                                                                                                                PRT;
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      Vertebrata;
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR456446; CA30332.1; -.
SEQUENCE 824 AA; 91333 MW; A74F186406041F7B CRC64;
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J.E., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huci
                                                                                                                                               NVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDAD
                                                                 LHCWITGWGALREGALRADAVALFYGWRNQGSETCCCPISNALQKVDVQLIPQDLCSEVY
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PQQITPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYT
                                                                                                                                                                                                                                                            EGEWFWQVSLHALGQGHICGASLISFNWLVSAAHCYIDDRGFRYSDFTQWTAFLGLHDQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGQGDGGDG----EEAEPEGMFKACE-----DSKRKARGYLRLVPLFVLL--ALLVLA
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                                                                                                                                                                                                                                EGEWPWQASLQVRGR-HICGGALIADRWVITAAHCFQED---SMASTVLWTVFLGKVWQN
                                                                                                                                                                                                                                                                                                                     -GVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCDCGLQG--PSSRIVGGAVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQLPRMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPG
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                                                                                                                                                                                                                                                                                                                                                                                                        -ACDGVKDCPNGLDERNCVCRA-TFQCKEDSTCISLPKVCDGQPDCLNGSDEEQCQE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1092; DB 2;
Pred. No. 7.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 330; Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 824;
                                                                                                          LILOKGEIRVINGTTCENLL
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Че В.J.,
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                                             Query Match
Best Local Sim
Matches 228;
                                                                                                                                                           Pfam; PF00431; CUB; 1.

Pfam; PF000431; CUB; 1.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00761; LDLRECEPTOR.

PROSITE; PS01180; CUB; 2:

PROSITE; PS01180; LDLRA 1; 1.

PROSITE; PS01209; LDLRA 2; 2.

PROSITE; PS50168; LDLRA 2; 2.

PROSITE; PS50134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00134; TRYPSIN SER; 1.
                                                                                                   Hydrolase;
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kamehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               GO; GO:0006508; P:proteolysis and peptidolysis; InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL receptor_A.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016021; C:integral to membrane; GO; GO:0004263; F:chymotrypsin activity; IEA. GO; GO:0008233; F:peptidase activity; IEA. GO; GO:0004295; F:trypsin activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to peptidase family S1. EMBL; BN000125; CAD67577.1; -. EMBL; AK131211; BAD18401.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINB=22722134; PubMed=12838346;

Puente X.S., Sanchez L.M., Overall C.M., I

"Human and mouse proteases: a comparative

Nat. Rev. Genet. 4:544-558(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type II transmembrane protein FLJ16088). Name=TMPRSS7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-CCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7RTY8
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Similarity
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                                                                                                      24
572 AA;
                                                                                                                                  Protease; Serine protease; Signal; Transmembrane
1 23 Potential.
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             ; LDL_receptor_A.
; Peptidase_S1.
; Peptidase_S1A.
                                                                                                      64041 MW;
                                                           21.4%;
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                                           95;
                                             Score 1004.5; DB Pred. No. 5.6e-61; 5; Mismatches 223
                                                                                                      type II transmembrane serine; 0458CBEA996EA285 CRC64;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                              UNKNOWN_1.
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                                              Indels 77;
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01-MAR-2004 (TrEMBLrel. 23
01-MAR-2004 (TrEMBLrel. 24
Mus musculus adult male co
enriched library, clone:B:
COAGULATION FACTOR XI.
Nature
[3]
                                                                     Carminci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                          MEDLINE=21085660; PubMed RIKEN FANTOM Consortium;
                                            SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                 STRAIN=C57BL/6J; TISSUE=Corpora qu
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                Mus musculus
                                                                                                                                                                          Name=B230219I23Rik;
                                                                                                                                                                                                                                        Q8BIK6;
                                                                                                                                                                                                                                                Q8BIK6
                  "Functional annotation of a full-length mouse
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          409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                VELIDQTLCVSTY-GIITSRMLCAGIMSGKRDACKGDSGGPLSCRRKSDGKWILTGIVSW
                                                                                                                                                                                                                                                                                                                                             IRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLS-SVEADGRIFGAGVVSW
                                                                                                                                                                                                                                                                                                                                                                  GHGCGRPNFPGVYTRVSNFVPWI
                                                                                                                                                                                                                                                                                                            GDGCAGRNKPGVYTRLPLFRDWI
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                                                                                                                                                                                                                                                                                                                                                                                                                        SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS--APGVQERRLKRIISHPFFNDFTFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                            CPDGSDEEGCTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLISPNWLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCTDHSDELNCSCDAGHQFTCKNKFC---KPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFRVPSPLVHIQLQCSSRLSDKPLLAEYGSYNISQPCPVGSFRCSSGLCVPQAQRCDGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP-GQFTCRTGRCIRKELRCDGWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPPKCKCTWKFQT-SLSTLGIALKFYNYSITKKSMKG-CEHGWWEINEHMYCGSYMDHQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPPNIDCTWNIEVPNNQHVKVRFKFF-YLLEPGVPAGTCPKDYVEINGEKYCGE--RSQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFVSTNNLMLVTFKSPHIRRLSGIRAYFEVIPEQKCENTVLVKDITGFEGKISSPYYPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRK----AQGTFNSPYYPGH
                                                                                                                                                                                                                                                                                                                                                                                                        SAAHCF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHFKLVAIVGYLIRLSIKSIQI-EADNCVTDSLTIYDSLLPIRSSILYRIC--EPTRTLM
                                                                                                                                                                                       (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
s adult male corpora quadrigemina cDNA, l
brary, clone:B230219I23 product:weakly s
                                                                                                                                             (Mouse).
etazoa; Chordata;
theria; Rodentia;
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                    N.A.
                                   TISSUE=Corpora qu
; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                        HGNRLSDFTPWTAHLGMYVQGNAKFVSP----VRRIVVHEYYNSQTFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CDGFRDCENGRDEQNC--TQSIPCNNRTFKCGNDICFRKQNAKCDGTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                          -RSSSALHRIIGGTDTLEGGWPWQVSLHFVGSAY-CGASVISREWLL
                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                 PRT;
                                                                                                         quadrigemina;
                                           quadrigemina
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                  cDNA collection.";
                                                                                                                                                                                           similar
                                                                                                                                                                                                    RIKEN
                                                                                                                                                        Euteleostomi;
                                                                                                                                               Murinae;
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SEQUENCE FROM N.A.

22 STRAIN-C57BL/61; TISSUB-Corpora quadrigemina;

23 STRAIN-C57BL/61; TISSUB-Corpora quadrigemina;

24 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

25 Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

26 Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume T.,

27 A Hayashida K., Hayatsu N., Hiraoka T., Hiraoka T., Hiraoka T.,

28 A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

29 A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

20 A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

28 A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

29 A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

20 A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

20 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

29 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

20 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

20 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

20 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

20 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

21 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

22 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

23 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

24 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

25 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

26 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

27 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

28 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

29 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

20 A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

2
                               Pfam; PF00431; CUB; 1.

Pfam; PF00089; Ldl recept a; 3.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR0072; CTYMOTRYPSIN.

PRINTS; PR007261; LDLARCEPTOR.

SMART; SM00042; CUB; 1.

SMART; SM00042; LDLa; 3.

SMART; SM00020; Tryp SPc; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS01209; LDLRA 2; 2.

PROSITE; PS012040; TRYPSIN HIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:2686594; B230219123Rik.
MGD; MGI:2686594; B230219123Rik.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:protecelysis and peptidoly
InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
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MEDLINE-20530913; PubMed=11076861;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Yamamoto R., Matsumoto H., Sakagucia S., Kegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium, the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/GJ; TISSUE=Corpora quadrigemina;
MEDLINE=20499374; PubMed=11042159;
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Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y
Hydrolase;
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Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamzaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Mrzakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.
                                                                                                                                                                                                                                                                                                                                    BAD18401 PRELIMINARY; PRT; 572 AA.
BAD18401;
12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ16088 fis, clone NTZRP7008435, weakly similar
3.4.21.-).
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Catarrhini; Hominidae;
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Best Local Sim
Matches 228;
                                                                                                                                                 PNTK PIG STANDARD; PRT; 1034 AA.

P98074;

P98074;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase)

Name=PRSS7; Synonyms=ENTK;

Sus scrofa (Pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Su
                                                                                                                                                                                                                                                                                                                                                                                                                     PIG
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Submitted (MAR‡2004) to the EMBL/GenBank/DDBJ databases EMBL; AK131211; BAD18401.1; -.

SEQUENCE 572 AA; 64041 MW; 0458CBEA996EA285 CRC64;
  YISOUENCE FROM N.A., AND PARTIAL SEC
TISSUE-Duodenal mucosa;
TISSUE-94327548; PubMed=8051081;
Matsushima M., Ichinose M., Yahagi
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                                                                                   SEQUENCE
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        Tsukada
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371 652 313 532 236

260

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541 826 482 767 422

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R PEAM; PRO0089; TRYPSIN; 1.

R PIRSF; PIRSFO01138; Enteropeptidase; 1.

R PRINTS; PR00722; CHYMOTRYPSIN.

R PRINTS; PR00720; MAMDOMAIN.

R SMART; SM001042; CUB; 2.

R SMART; SM001042; CUB; 2.

R SMART; SM00107; MAM; 1.

R SMART; SM00107; SEA; 1.

R SMART; SM00200; SEA; 1.

R SMART; SM00200; SEA; 1.

R SMART; SM00200; STAP; 1.

R SMART; SM00200; Tryp SPC; 1.

PROSITE; PS001180; CUB; 2.

PROSITE; PS001180; CUB; 2.

PROSITE; PS00109; LDLRA_1; 2.

PROSITE; PS00109; LDLRA_2; 2.

PROSITE; PS00740; MAM_1; 1.

PROSITE; PS00740; MAM_2; 1.

PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000859; C
InterPro; IPR002172;
InterPro; IPR002189; M
InterPro; IPR001254; P
InterPro; IPR001314; P
InterPro; IPR001314; P
InterPro; IPR011163; P
InterPro; IPR001082; S
                                                                                                                                                                                                                                                                Pfam, PF00431;
Pfam, PF00057;
Pfam, PF00629;
Pfam, PF01390;
Pfam, PF00530;
Pfam, PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Inoue H., Takahashi T., Takahashi K.;
                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01
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CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-[-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type II membrane protein (Probable) PTM: The chains are derived from a single precursor that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (heavy) chain, and a r
SUBCELLULAR LOCATION:
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SUBUNIT: Het
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PF00057; Ldl_recept_a; 2.
PF00629; MAM; 1.
PF01390; SEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    D30799; BAA06459.1;
P98072; 1EKB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterization of
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Peptidase_S1A.
Pept_S1A_enterop.
Pept_Ser_Cys.
SEA.
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protease;
  Signal-anchor;
           Hydrolase;
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  ; Lipoprotein; Transmembrane;
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Query Match
Best Local &
Matches 258
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                                       IKEELIQGIEANKSSQLVAFHIDVNSIDITESLENYSTTSPSTTSDKLTTSSPPATPGNV
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-LP---PRARSLKSFVV----TSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFT
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Charge relay system (B.
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By similarity.
N-linked (GlCNAC...)
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                                                                                                                                                                                                                                                                             Score 724; DB 1;
Pred. No. 3.1e-41;
5; Mismatches 330
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Signal-anchor for type II membrane
protein (Potential).
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Enteropeptidase non-catalytic
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e (Potential).
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01-CCT-2003 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
Polyserase-IB protein.
Homo sapiens (Human).
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Best Local Similarity
Matches 132; Conserv
                                                                                                            Q7Z411
Q7Z411;
Q7Z411;
Q7Z412
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
Polyserase-IA protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chord
Mammalia; Butheria; Prima
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SMART; SM00010; Tryp SPc; 2.

PROSITE; PS50068; LDLRA; 1.

PROSITE; PS50240; TRYPSIN DOM; 2

PROSITE; PS00134; TRYPSIN_HIS; UI

PROSITE; PS00135; TRYPSIN_HSER; 2
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MEROPS; S01.969; -..

G0; G0:0004295; F:trypsin activity; IEA.

G0; G0:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002172; LDL_receptor A.

InterPro; IPR002173; LDL_receptor A.

InterPro; IPR0012134; Peptidase_S1.

Pfam; PF00057; Ldl_recept_a; 1.

Pfam; PF00089; Trypsin; 2.
 TISSUE=Liver;
MEDLINE=22784742; PubMed=12886014;
Cal S., Lopez-Otin C.;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                          SEQUENCE FROM N.A.
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                                                                                           NCBI_TaxID=9606;
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"Polyserase-I, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22784742; PubMed=12886014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPWQASLRE-NKEHFCGAAIINARWLVSAAHCFNE----FQDPTKWVAYVGATYLSGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPGNSFSCGNSQCVTKVNPECDDQEDCSDGSDEAHCECGLQPAWRMAGRIVGGMEASPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; Serine protease.
855 AA; 91352 MW; 8AF2759D9740CF3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad. Sci. U.S.A. 100:9185-9190(2003)
947; CAD35759.1; -.
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                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%;
45.7%;
                                                                                                                  Primates;
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tease domains
                                                                                                                                                                                        25,
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Last seq
Last ann
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Pred. No. 1.8e-40;
2; Mismatches 96;
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Indels Length

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Gaps

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685 213 855;

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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                    sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM: PF00057; Ldl_recept_a
Pfam: PF00057; Ldl_recept_a
Pfam: PF00089; Trypsin: 3.
SWART; SM00192; LDI--
PFC--
SMART; SM000192; LDI--
                                                                                                                                                                                                                                       ENTK BOVIN STANDARD P98072;
01-FEB-1996 (Rel. 33, C 01-FEB-1996 (Rel. 33, L 01-OCT-2004 (Rel. 45, L
                                                                                                                                                                                                                                                                                                         LT 23
_BOVIN
                                                                                                                                                                                                              01-OCT-2004 (Rel. 45, Last
Enteropeptidase precursor
Name=PRSS7; Synonyms=ENTK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00192; LĎLa; 1.
SMART; SM00020; Tryp_SDc; 3.
PROSITE; P850068; LDLRA 2; 1.
PROSITE; P850240; TRYPSIN_DOM; 3.
PROSITE; P850134; TRYPSIN_HIS; UNKNOWN_3.
PROSITE; P800135; TRYPSIN_SER; 2.
Hydrolase; Protease; Serime protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.357; -. MEROPS; S01.358; -. MEROPS; S01.969; -.
                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis;
InterPro; IPR002172; LDL receptor A.
InterPro; IPR00154; Peptidase SI.
SEQUENCE OF 801-1035
MEDLINE=94043122; Pul
                                                    protease
                                                                                                         TISSUE=Duodenum;
                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                             Bovinae; Bos.
                                                                                                                                                                          Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                     Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.; "Enterokinase, the initiator of intestinal digestion, i protease composed of a distinctive assortment of domain proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
                                                                                        MEDLINE=94329561; PubMed=8052624;
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independent seri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQA-RVVGGTDADEGE
                                                                                                                                                                                                                                                                                                                                                               SGGPLVCEEPSGRFFLAGIVSWGIGCAEARRPGVYARVTRLRDWILEAT
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                                                                                                                                                                                                                                                                                                                                                                                       SGGPLSSVEADGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWIKENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease;
1059 AA;
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    I, a human polyprotease with the ability to generate
serine protease domains from a single translation

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                                                                                                                                                                                                                                                                                                STANDARD;
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)35 FROM N.A., AI
PubMed=8226855;
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                                                                                                                    AND PARTIAL
                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
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114020 MW; 17D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%;
45.7%;
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t annotation updat
(EC 3.4.21.9) (Er
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Pred. No. 2.3
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                                                                                                                     SEQUENCE.
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            PARTIAL
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..9) (Ente:
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             SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grant K.L., Light A., McCoy J.M.;
"Cloning and functional expression of
subunit of bovine enterokinase.";
J. Biol. Chem. 268:23311-23317(1993).
EMBL; U09859; AAB40026.1; -. EMBL; L19663; AAA16035.1; -.
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MEDLINE=92189715;
Light A., Janska I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 801-827.
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                                                                  send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rUNCTION: RESPONSIBLE for initiating activation of pancreatic proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases.

CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in trynsinogen
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SP
                                                                                                                                                                                                                                          cleaved by a trypsin-like protease.
SIMILARITY: Belongs to peptidase family S1
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 2 LDL-receptor class
SIMILARITY: Contains 1 MAM domain.
SIMILARITY: Contains 1 SEA domain.
SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trypsinogen.
SUBUNIT: Heterodimer of a catalytic (light) cha
multidomain (heavy) chain linked by a disulfide
SUBCELLULAR LOCATION: Type II membrane protein
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P98072-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P98072-2;
                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                P98072-2; Sequence=VSP_005386; PECIFICITY: Intestinal brush b chains are derived from a sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=Displayed,
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                                                                                                                                                                                                                                                                                                                                                                                                                           border.
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InterPro; IPR000082; InterPro; IPR001190; Pfam; PF00431; CUB; 2 Pfam; PF00057; Ldl_re PRINTS; P PRINTS; P PROSITE; PROSITE; PIRSF; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; MEROPS; S01.156; InterPro; A43090; A43090. 1EKB; X-ray; A=788-800, pP00431; CUB; 2.
; pF00057; Ldl recept_a; 2.
; pF00629; MAM; 1.
; PF01390; SEA; 1.
; PF00530; SRCR; 1.
; PF00089; TYYPSin; 1.
; PF00089; TYYPSin; 1. PF00431; PF00057; PF00629; PF01390; PF00530; PF00089; 3; PR00722; CHYMOTRYPSIN.
5; PR00261; LDLEECEPTOR.
12; PS01180; CUB; 2.
12; PS01109; LDLRA 1; 2.
12; PS50068; LDLRA 2; 2. ; IPR000998; ; IPR001254; ; IPR001314; ; IPR011163; ; IPR009003; IPR000859; CUB.
IPR002172; LDL_receptor_A
IPR000998; MAM. ; Peptidase_S1. ; Peptidase_S1A. ; Pept_S1A_enterop. ; Pept_Ser_Cys. Srcr_receptor B=801-1035

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PS50060;
PS50024;
PS00420;
PS50287;
PS50240;
PS00134;
PS00135;
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HAM 2; 1.
SEA; 1.
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SRCR 2; 1.
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CUB 2.

CUB 2.

LDL-receptor clas
SRCR.

Serine protease.
Charge relay syss
Similarity.
By similarity.

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Extracellular (Potential).
SEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (GlcNAc.)
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                              LNETVEFKVSFYGFKNQILSDIALDDISLTYGICNVSVYPEPTLVPTPPPELP---TDCGG
                                                                                     LPLDPTPEQACLSFWYYMYGENVYKLSINISSDQ---NMEKTIFQKEGNYGQNWNYGQVT
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  CHARACTERIZATION.
MEDLINE=20359740; PubMed=10880574; DOI=10.1073/pnas.150149097;
                                                                                                                                            "Localization of the
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              PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0261; LDLRECEPTOR.
PROSITE; PSS0038; FZ; 2.
PROSITE; PSS0038; FZ; 2.
PROSITE; PSS0068; LDLRA_2; 6.
PROSITE; PSS0068; LDLRA_2; 7.
PROSITE; PSS0020; SRCR_1; FALSE_NEG.
PROSITE; PSS0287; SRCR_2; FALSE_NEG.
PROSITE; PSS0287; SRCR_2; FALSE_NEG.
PROSITE; PSS0240; TRYPSIN_DOM; 1.
PROSITE; PSS0240; TRYPSIN_DOM; 1.
PROSITE; PSS00135; TRYPSIN_ESR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000024; Fz domain.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR002173; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR00903; Peptidase S1A.
InterPro; IPR00903; Peptidase S1A.
InterPro; IPR009013; Peptidase S1A.
InterPro; IPR00903; Peptidase S1A.
InterPro; IPR001903; Peri Srcr receptor.
IPR01392; Fz; 2.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 605236; -. 60; GO:0005887; GO:0006622; GO:0006623; GO:000653; GO: GO:0008517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is modified and this statement into tremoved. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      natriuretic peptide-converting enzyme.";
Proc. Natl. Acad. Sci. U.S.A. 97:8525-8529(2000)
-!- FUNCTION: Converts Pro-ANP to ANP. Cleaves E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.019; -.
Genew; HGNC:19012; CORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yan W., Wu F., Morser J., Wu Q.; "Corin, a transmembrane cardiac serine protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 605236; ...
GO:0005887; C:integral to plasma membrane; TAS.
GO:0004252; F:serine-type endopeptidase activit
GO:0006629; F:lipid metabolism; TAS.
GO:000653; P:morphogenesis; TAS.
GO:000658; P:proteolysis and peptidolysis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type II membrane protein TISSUE SPECIFICITY: Highly expressed in heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between Arg-123 and Ser-124.
SUBCELLULAR LOCATION: Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01392; Fz; 2.
PF00057; Ldl_recept_a; 6.
PF00089; Trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF133845; AAD31850.1; -. AF113248; AAF21966.1; -.
              134
134
268
341
378
378
378
657
657
690
892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
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P:regulation of blood pressure;
           1042
259
304
340
340
375
415
513
614
653
653
698
843
                                                                                                                                                                                                                                                                                                                                                                                                                                              665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Serine protease;
                                                                                                                                                                                                                                                    LDL-receptor class I
LDL-receptor class I
LDL-receptor class I
     SRCR.
Serine
Charge
Charge
Charge
                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
                                                                                                                                         LDL-receptor class LDL-receptor class LDL-receptor class
                                                                                                                                                                                                                                                                                                                                                                  FΖ
                                                                                                                                                                                                                                                                                                                                                                                        protein (Poter
Extracellular
     e relay system e relay system.
                                                                                       protease
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Best Local S
Matches 210
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.8%; ll Similarity 28.2%; 210; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCSVIQTSCQEGDQRCLYNPCLDSCG--GSSLCDPNNSLNNCSQCEPITL-ELCMNLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHDCVDKSDEVNCS--CHSQGLVECR----NGQCIPSTFQCD----GDEDCKDGSDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDAD-----
DYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEI 768
                                   KWVLTVAHCF-EGR----ENAAVWKVVLGINNLDHPSV-FMQTRFVKTIILHPRYSRAVV
                                                                                                                                                                              WQEILSQLACKOMGLGEPSVTKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQSCES
                                                                                                                                                                                                                                                  DELECANHACVSRDLWCDGEADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHVCADG
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                                                                  NWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTF
                                                                                                     RSKISLLCTKQ--DCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSBPSGHICGCVLIAK
                                                                                                                                     KEDCSDGSDEKDCDCGLRSFTR-QARVVGGTDADEGEWPWQVSLHALGQGHICGASLISP
                                                                                                                                                                                                                                                                                                                       RCDGQADCDDDSDEENCGCKERDLWECPSNKQCLKHTVICDGFPDCPDYMDEKNCSFCQD
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; Pred. No. 3.1e-39; 
97; Mismatches 265; Indels 17
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By similarity.
By similarity.
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N-linked (GlCNAC. .) (Poten N-linked M-linked N-linked M-linked N-linked M-linked M-linked N-linked M-linked M-linked
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A Langenickel T., Pagel I., Buttgereit J., Tenner K., Lindner

Millenbrock R., Dietz R., Bader M.;

Willenbrock R., Dietz R., Bader M.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

C -I- SIMILARITY: Belongs to peptidase family S1.

EMBL; AY251285; AAO86772.1; -.

EMBL; AY251285; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

R GO; GO:0004263; F:chymotrypsin activity; IEA.

R GO; GO:0005044; F:scavenger receptor activity; IEA.

R GO; GO:0004265; F:trypsin activity; IEA.

R GO; GO:0007275; P:development; IEA.

R GO; GO:0007275; P:development; IEA.

GO; GO:000508; P:proteolysis and peptidolysis; IEA.
                                                                                                  Query Match
Best Local Similarity
Matches 210; Conserv
                                                                                                                                                                                       SMART; SM00202; SR; 1.
SMART; SM00202; Tryp SPC; 1.
SMART; SM00320; Tryp SPC; 1.
PROSITE; PS50038; FZ; 2.
PROSITE; PS500368; LDLRA 1; 6.
PROSITE; PS500368; LDLRA 2; 7.
PROSITE; PS50287; SRCR Z; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS50240; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                             Pfam; PF01392; Fz; 2.

Pfam; PF00037; LdI_recept_a; 6.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00726; LDLRECEPTOR.

SMART; SM00063; FRI; 2.

SMART; SM00192; LDLa; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q80YN4;
Q80YN4;
01-JUN-2003
01-JUN-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000024; Fz domain.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR0012174; LDL receptor A.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR009903; Pept Ser Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Bukaryota; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR009003; InterPro; IPR001190;
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265 LASCDE--RGSDLVTVYNTL---SPMEPHALVQLCGTYPPSYNLTFH-----
                                             TFQCDGDEDCKDGSDEENCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRSFD
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                                                                                                                                                                              Protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                              AA;
                                                                                                   14.8%; Score 694.5; DB 2; 28.7%; Pred. No. 3.7e-39; tive 80; Mismatches 259;
                                                                                                                                                              Serine protease.
122635 MW; 3BA2
                                                                                                                                                                                                                                                                                                                                                                                                               Srcr_receptor
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Last sequence update)
Last annotation updat
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                3BA2706CBE81157F CRC64;
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                                                                                                      Indels
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                                                                                                                                    1111,
                                                                                                      183;
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                                                                                                      Gaps
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RESULT QREAN9
ID Q8
DT Q8
DT 011
DT 011
DT 011
DT 011
DT 011
DT 011
CR Nu 01
CR Nu 02
CR Nu (11
CR RC STERN (22
CR NU (22
CR NU CR CR NU (22
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Q8CAN9;
01-MAR-2003
                                                                                                    STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:Al30097D21 product:protease, serine, 7 (enterokinase),
full insert sequence. (Fragment).
   STRAIN=C57BL/6J; (MEDLINE=21085660;
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                     SEQUENCE FROM
                                                                    "High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                 Name=Prss7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITVRFHSDQSYTDTGFLAEYLSYDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSDE
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                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                     N.A.
TISSUE=Thymus; PubMed=11217851;
                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EHSKERCESVL----GIVGLQWPED---
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                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae
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     InterPro;
InterPro;
InterPro;
 Pfam; P
Pfam; P
PRINTS;
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InterPro;
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                           InterPro;
                                                                                                        InterPro;
                 PF00530;
                                                       MAM;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new grenome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Thymus; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Thymus;
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REQUENCE FROM N.A.

RESTRAIN=C57BL/6J; TISSUB=Thymus;

RC STRAIN=C57BL/6J; TISSUB=Thymus;

RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Alzawa K., Hanagaki T., Harra A., Hashizume W.,

RA Kurida S., Puruno M., Hanagaki T., Hiraoka T., Hirozane T.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Momura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Shiraki T., Sogabe Y., Tagami M.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RI Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RI Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RI Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RI Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RI SIMIIARITY: Belongs to peptidase family S1.

CC -!- SIMIIARITY: Contains 1 MAM domain.

CC EMBL, AKO38356; BAC29973.1; --. .

Tagami ka T., s: 3

); MGI:1197523; Pr887.
GO:0016020; C:membrane; IEA.
GO:0004263; F:chymotrypsin activity; IEA.
GO:0016301; F:kinase activity; IEA.
GO:0008233; F:peptidase activity; IEA.
GO:0005044; F:scavenger receptor activity;
GO:0004295; F:trypsin activity; IEA.
GO:0006508; P:proteolysis and peptidolysis;

peptidolysis; IEA IEA.

o; IRR002172; LDL receptor A.
c; IPR00298; MAM.
i; IPR001254; Peptidee IPR001314; IPR009003; IPR001190; Srcr_receptor Peptidase_S1A Pept_Ser_Cys.

SRCR; 1. Trypsin; CHYMOTRYPSIN

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DR SMART; SM00137; MAM; 1.

DR SMART; SM001202; SR; 1.

DR SMART; SM000202; Tryp_SPc; 1.

DR SMART; SM000202; Tryp_SPc; 1.

DR SMART; SM000202; Tryp_SPc; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS01209; LDLRA_2; 1.

R PROSITE; PS50068; LDLRA_2; 1.

R PROSITE; PS50060; MAM_2; 1.

R PROSITE; PS50060; MAM_2; 1.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_HS; UNKNOWN_1.

R PROSITE; PS00134; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

M Glycoprotein; Hydrolase; Kinase; Protease; Serine pro
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Best Local
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                                             HUMAN
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                                                                                                                                                                                                                                                                                              H---ICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLK
                                                                                                                                DGRIFGAGVVSWGDGCAGRNKPGVYTRLPLFRDWI 849
                                                                                                                                                                                                                                                RIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQY
                                                                                                                                                                                                                                                                                                                                       LQCSQDSLILLQCNHKS-----CGEKKVTQKVSPKIVGGSDAQAGAWPWVVALYHRDRS
                                                                                                                                                                                                                                                                                                                                                        PECDGKE----DCSDGSDEKDCDCGLRSFTRQA--RVVGGTDADEGEWPWQVSLHALGQG
                                                                                                                                                                                                                                                                                                                                                                                                 EVC----
                                                                                                                                                                                                                                                                                                                                                                                                                           GKCLSKSQQCNGKDDCGDGSDEASCP-----KVNVVTCTKHTYRCLNGLCLSKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELNC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNIQLHFQEFDLEN-----INDVVEVRDGGEFDSLLLAVYTGPGPVKDLFSTTNRMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QHVKVRFKFFYLLBPGVPAGTCPKDYVEI--NGE-----KYCGERSQFVVTSNSNKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVFNAFRNRGCSTIALDDISLTNGICSQSPYPEPTLVPTPPP---------
                                                                                                      NNRWFLVGVTSFGVQCALPNHPGVYVRVSQFIEWI
                                                                                                                                                              NGSTVDVLKEADVPLISNEKCQQQLPEYNITESMICAGYEEGGIDSCQGDSGGPLMCQE-
                                                                                                                                                                                        GGTGALILQKGEIRVINQTTCENLLPQ-QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEA
                                                                                                                                                                                                                     QIVINPHYDRRRKVNDIAMMHLEFKVNYTDYIQPICLPEENQIFIPGRTCSIAGWGYDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EASCVRFLNGTRSNNGLVOFNIHS----IWHI----ACAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIFTTNMETRRKGFKANFTSGYYLGIPEPCQDDEFQCKDGNCIPLGNLCDSYPHCRDGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRFHSDQSYTDTGFLAEYLS---YDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNTERRHPGFEATFFQLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNN
                                                                                                                                                                                                                                                                               TDRLLCGASLVSSDWLVSAAHCVYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777 AA; 87314 MW; A18E2F4ECF06D3A8 CRC64;
 (Rel. 33, Created)
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                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELP--TDCGGPFELWEPNSTFSSPNFPDKYPNQASCIWNLNAQRG
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Pred. No. 1.3e-38;
                              1019
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REDINE-20283799; PubMed=10830953;

RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

RA Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,

RA Park H.-S., Toyda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,

RA Park H.-S., Toyda A., Ishii K., Totoki Y., Taudien S., Blechschmidt K.,

RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,

RA Polley A., Menzel U., Delabbar J., Kumpf K., Lehmann R., Patterson D.,

RA Rosenthal A., Kudoh J., Schilhabel M., Schudy A., Zimmermann W.,

RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,

RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

Minoshima S., Shimizu N., Nordsiek R., Hornischer K., Brandt P.,

NA Minoshima S., Shimizu N., Nordsiek R., Hornischer K., Brandt P.,

RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,

RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

"The DNA sequence of human chromosome 21.";

Nature 405:311-319(2000).
                          trypsinogen.

I SUBUNIT: Heterodimer of a catalytic (light) chain and a multidomain (heavy) chain linked by a disulfide bond.

SUBCELULAR LOCATION: Type II membrane protein (Probable).

ITSSUE SPECIFICITY: Intestinal brush border.

FINSUE SPECIFICITY: Intestinal brush border.

ITSSUE SPECIFICITY: Intestinal brush border.

INTESTITE COATION: Type II membrane protein (Probable).

INTESTITE SPECIFICITY: Intestinal brush border.

INTESTITE SPECIFICITY: Intestinal brush border.

INTESTITE SPECIFICITY: Intestinal brush border.

INTESTITE SPECIFICITY: Are a cause of enterokinase deficiency characterized by diarrhea and failure to thrive.

INTESTITE SPECIFICITY: Belongs to peptidase family S1.

INTESTITE SIMILARITY: Contains 2 LUL-receptor class A domains.

INTESTITE SIMILARITY: Contains 1 MAM domain.

INTESTITE SIMILARITY: Contains 1 SER domain.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-94329561; PubMed-8052624;

Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.;

Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.;

Rinterokinase, the initiator of intestinal digestion, is a mosaic protease composed of a distinctive assortment of domains.";

Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).

-I- FUNCTION: Responsible for initiating activation of pancreatic proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases.

-I- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=21606074; PubMed=11719902;
Holzinger A., Maier E.M., Buck C., Mayerhofer P.U., Kappler
Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher
"Mutations in the proenteropeptidase gene are the molecular
congenital enteropeptidase deficiency.";
cm. J. Hum. Genet. 70:20-25(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95234679; PubMed=7718557; Kitamoto Y., Veile R.A., Donis-Keller H., Sa "cDNA sequence and chromosomal localization proteolytic activator of trypsinogen."; Biochemistry 34:4562-4568(1995).
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Eukaryota; Metazoa;
Mammalia; Butheria;
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05-JUL-2004 (Rel. 44, Last annotation update)
Enteropeptidase precursor (EC 3.4.21.9) (Ente
Name=PRSS7; Synonyms=ENTK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mayerhofer P.U., Kappler M.-B., Sadler J.E., Roscher
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Dagand E.,
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produced through a collaboration

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Pfam; PPO0431; Cub; a. Recept_a; 2. Ream; PF00057; Ldl recept_a; 2. Refam; PF00059; SEA; 1. Refam; PF001390; SEA; 1. Refam; PF001390; SRCR; 1. Pfam; PF001390; SRCR; 1. Pfam; PF00089; Trypsin; 1. PR Pfam; PF00089; Trypsin; 1. DR PRINTS; PR00722; CHYMOTRYESIN. PRINTS; PR00726; LDLRECEPTOR. PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR000261; LDLRA_1; 2. DR PROSITE; PS01180; CUB; 2. DR PROSITE; PS01069; LDLRA_1; 2. DR PROSITE; PS010709; MAM[]; 1. DR PROSITE; PS00704; MAM_2; 1. DR PROSITE; PS00704; MAM_2; 1. DR PROSITE; PS00704; SECR_1; FALSE_NEG. PROSITE; PS0024; SECR_1; FALSE_NEG. PROSITE; PS0024; SRCR_2; 1. DR PROSITE; PS0024; SRCR_2; 1. PROSITE; PS00237; SRCR_2; 1. PROSITE; PS00237; SRCR_2; 1. PROSITE; PS00134; TRYPSIN_DS; 1. PROSITE; PS00135; TRYPSIN_SER; 1.
       EMBL; U09860; AAC50138.1; -.
EMBL; Y19124; CAB65555.1; JOII
EMBL; Y19125; CAB65555.1; JOII
EMBL; Y19126; CAB65555.1; JOII
EMBL; Y19128; CAB65555.1; JOII
EMBL; Y19128; CAB65555.1; JOII
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
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HGNC:9490; PRSS7.
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                                                                       Hydrolase; Lipoprotein; Myristate; Repeat; se; Signal-anchor; Transmembrane; Zymogen.
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; Pept_S1A_enterop.
; Pept_Ser_Cys.
; SEA.
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Enteropeptidase catalytic chain.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
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                                                     GDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDG-----KEDCSDGS-----D
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                                                                                                                                                                                                                                                                                                                                 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP
                     GLGSGNSSKPIFST---
                                                                                         TTNNNGLVRFRIQSIW----HTACAEN
                                                                                                                                                           ANFTTGYHLGIPEPCKADHFQCKNGECVPLVNLCDGHLHCEDGSDEADCV----
                                                                                                                                                                                             AEYLS---YDSSDPCPG-QFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQF---
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S -> P (in Ref. 3).
SQCCLQDSLIRLQCNHKS -> SQCCL
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Charge relay system (N-myristoyl glycine By similarity.

By similarity.
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Pred. No. 3.6e
30; Mismatches
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N-linked
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N-linked
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Serine
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Extracellular (Potential).
SEA.
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                   -DGGPFVKLNTAPDGHLILTPSQQCLQDSLIRLQCN
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les 202;
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(Potential).
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ENTK MOUSE
P97435;
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Enteropeptidase (EC 3.4.21.9) (Enterokinase).
Name=Prss7; Synonyms=Entk;
Mus minarilia (Mus.--)
                                                                                                                                                                                                                                     EMBL; U73378; AAB37317.1; HSSP; P98072; 1EKB. MEROPS; S01.156; -.
                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Duodenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                      <del>+</del> <del>+</del> <del>+</del>
                                                                                                                                                                                                                                                                                                                        ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., S "Structure of murine enterokinase (enteropeptidase) small intestine during development."; Am. J. Physiol. 274:6342-6349(1998).

-I- FUNCTION: Responsible for initiating activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98147142; PubMed=9486188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                    entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                PTM: The chains are derived from a single precursor that cleaved by a trypsin-like protease (By similarity).

SIMILARITY: Belongs to peptidase family S1.

SIMILARITY: Contains 2 CUB domains.

SIMILARITY: Contains 2 LDL-receptor class A domains.

SIMILARITY: Contains 1 MAM domain.

SIMILARITY: Contains 1 SRA domain.

SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Responsible for initiating activation of pancreatic proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases (By similarity).

CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type II membrane PTM: The chains are derived from a sing
                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                                                                                                                                                          trypsinogen.
SUBUNIT: Het
                                                                                                                                                                                                                                                                                                                                                                         multidomain (heavy)
                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1069
                                                                                  moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                There are no restrictions ong as its content is in
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and expression
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     SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01180; LDLRA_2; 2.

PROSITE; PS05068; LDLRA_2; 2.

PROSITE; PS50068; MAM_1; 1.

PROSITE; PS500740; MAM_2; 1.

PROSITE; PS500740; MAM_2; 1.

PROSITE; PS50024; SEA; 1.

PROSITE; PS50024; SECR_1; FALSE_1

PROSITE; PS500240; SRCR_2; 1.

PROSITE; PS500240; TRYPSIN_DOM; 1.

PROSITE; PS500134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.
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InterPro;
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SMART; SM00192;
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PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR00020; MAMDOMAIN.
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Pfam; PF00089; Trypein; 1.
PIRSF; PIRSF001138; Enteropeptidase;
PRINTS; PR00722; CHYMOTRYPSIN.
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InterPro; IPR00085
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PF00057; Ldl_recept_a;
PF00629; MAM; 1.
PF01390; SEA; 1.
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IPR001190;
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   Hydrolase;
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LDLa; 2.
MAM; 1.
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Pept_StA_enterop.
Pept_Ser_Cys.
SEA.
STOR_receptor.
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 SRCR.
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Enteropeptidase catalytic chain.
Cytoplasmic (Potential)
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Best Local S
Matches 186
                                                 CORI MOUSE
Q9Z319;
16-OCT-2001
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Atrial natri
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Name=Corin;
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                                     -2001 (Rel. 40, Created)
-2001 (Rel. 40, Last sequence update)
-2004 (Rel. 44, Last annotation update)
-2004 (Rel. 44, Last annotation update)
natriuteric peptide-converting enzyme (BC 3.4
ting enzyme) (Corin) (Low density lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                           -NNRWFLVGVTSFGVQCALPNHPGVYVRVSQFIEWI
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               Synonyms=Crn,
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            Lrp4;
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ein receptor related
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     PRINTS; PRO0089; Trypsin; 1.

PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PR007261; LDLRECEPTOR.

SMART; SM00063; FRI; 2.

SMART; SM00192; LDLa; 7.

SMART; SM00192; Tryp_SPC; 1.

SMART; SM00202; SR; 1.

SMART; SM00202; SR; 1.

SMART; SM00202; Tryp_SPC; 1.

PROSITE; PS50038; FZ; 2.

PROSITE; PS50068; LDLRA_1; 6.

PROSITE; PS50068; LDLRA_2; 7.

PROSITE; PS500420; SRCR 1; FALSE NEG.

PROSITE; PS500420; TRYPSIN DOM; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS50134; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

Glycoprotein; Hydrolase; Repeat; Serin
DOMAIN
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InterPro; IPR002172; L
InterPro; IPR001254;
InterPro; IPR001254; P
InterPro; IPR001314; P
InterPro; IPR009003; P
InterPro; IPR001190; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- FUNCTION: Converts pro-ANP to ANP. Cleaves pro-Joetween Arg-122 and Ser-123 (By similarity).
-:- SUBCELIULAR LOCATION: Type II membrane protein.
-:- TISSUE SPECIFICITY: Highly expressed in heart.
-:- SIMILARITY: Belongs to peptidase family S1.
-:- SIMILARITY: Contains 2 frizzled (FZ) domains.
-:- SIMILARITY: Contains 7 LDL-receptor class A dom.
-:- SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDIINE-98429596; PubMed=9756624;

Tomita Y., Kim D.-H., Magoori K., Fujino T., Yamamoto T.T.

"A novel low-density lipoprotein receptor-related protein
"A novel low-density lipoprotein is abundant in heart.";

membrane protein-like structure is abundant in heart.";
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                                                                                                                                                                                                   Glycoprotein; Hydrolase; Transmembrane.
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HSSP; P01130; 1AJJ.
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Mammalia; Eutheria;
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PF00057; Ldl_recept_a; 6.
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Rodentia;
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; LDL receptor A.
; Peptidase_S1.
; Peptidase_S1A.
; Pept_Ser_Cys.
; Srcr_receptor.
                                   Extracellular (Potential).
FZ 1.
LDL-receptor class A 1.
LDL-receptor class A 3.
LDL-receptor class A 3.
LDL-receptor class A 4.
FZ 2.
LDL-receptor class A 5.
LDL-receptor class A 6.
LDL-receptor class A 6.
LDL-receptor class A 7.
  Serine
Charge
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or for type
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Pred. No. 7.1e-
67; Mismatches
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Last sequence update)
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS01209; LDLRA_1; 8.
PROSITE; PS01068; LDLRA_2; 2.
PROSITE; PS50264; TRYPSIN_DOW; 1
PROSITE; PS50244; TRYPSIN_HIS; UI
PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR001214; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00760; 1EZX.

MEROPS; S01.049; -.

G0; G0:0016020; C:membrane; IEA.

G0; G0:0004263; F:chymotrypsin activity; IEA.

G0; G0:0008233; F:peptidase activity; IEA.

G0; G0:000824; F:scavenger receptor activity;

G0; G0:0005044; F:scavenger receptor activity;

G0; G0:0004295; F:trypsin activity; IEA.

G0; G0:0004295; P:proteolysis and peptidolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR001190; Srcr_receptor.
Pfam; PF00057; Ldl recept a; 4.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Xenopus laevis.";
Gene 252:209-216(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus Îaevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=20363741; PubMed=10903452;
Yamada K., Takabatake T., Takeshima K.;
"Isolation and characterization of three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Embryonic serine protease-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Xesp-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |- SIMILARITY: Belongs to |
MBL; AB038497; BAB08217.1;
                                                                                                                                                                                                                                                                                                                                                                 365
                   603
                                              429
                                                                                                                                549
                                                                                                                                                                                                                                                                                                                                                                                              170;
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                              ADFQLQVYSTSVSAWLPVCSDYWNDDFGRFACQDFGYNGSSYNRYDTLMSPYAPNGYFKL
                                                                                                                                                             AYOMCOGVROCYYGODERNCVTATTTTATTTSPPTCQIYCMVFMYYYTCIYAYOMCOGVR
                                                                                                                                                                                         LFWVCDSVNDCGDNSDEQGC-----
                                                                                                                                                                                                                                                                            NCATKTPSIPTCQMYC--SYTSTCIYGYQI-----
                                                                                                                                                                                                                                                                                                        FVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTG------
                                                                                                                                                                                                                                                                                                                                     DCPYGDDERNCATKTPSTPTCQMYCSYYY-----TCIYGYQICNGVQDCPYGDDER
                                                                                                                                                                                                                                                                                                                                                                DCTWN-----IEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVBINGEKYC---GERSQ
                                                                                                                               DCGDGSDEASC-PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDC----
                                                                                                                                                                                                                   PTCQLYCSYYYTCIYAYQICNGVLDCPFVDDERNCVIATTSTPTCQIYCWDFMFDYTCIY
                                                                                                    QCYYGDDELNCDTRTTTAYCEK---RCGSSVSCVLSSQWCDGVSDCPYGEDEMSCVSLYP
                                                                                                                                                                                                                                              ------RCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease;
767 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    %; Serine pr
86001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           13.7%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease.
W; E0566A38796DE96E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 639.5; DB 2
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family
  -DCGLRSFTRQARVVGGTDADEGEWPWQVSL
                                                                                                                                                                                        -SCPAQTFRCSN----GKCLSKSQQCNGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel
                                                                                                                                                                                                                                                                                                                                                                                               215;
                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                            CNGVQDCAYGDDERNCATKTPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine
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                                                                                                                                                                                                                                                                                                                                                                                                                          767;
                                                                                                                                                                                                                                                                                                                                                                                              183;
                                                                                                                                                                                                                                                  -NKFCKP
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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311 548 371 462 251 503

Search completed: November 29, 2004, 08:32:31 Job time : 150.315 secs

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Result
No.
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Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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Perfect score: 3789
Sequence: 1 MAEERVVMLPPRARSLKSFV......PGVYTRLPLFRDWIKENTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     2379
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seq length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uniprot_02:*
uniprot_sprot:*
uniprot_trembl:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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                                                                                           62.8
59.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length DB
        GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
     ST14 HUMAN
ST14 MOUSE
BAC55125
Q9JJI7
Q9WC1
Q6WC1
Q6GE4
Q9DGR1
Q6GEV0
Q7RTY8
BAD18401
Q8B1K6
Q6PP94
AAH57674
TMS6 HUMAN
Q6UXDB
AAQ88764
Q6UXDB
AAQ88764
Q6IXZB
CAG30332
ENTK PIG
Q7Z411
CORI HUMAN
Q8CYN4
Q8CYNA
Q8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Ofice2 homo sapien
Cag30332 homo sapien
Cag30332 homo sapien
P98074 sus scrofa
Q7z410 homo sapien
Q7z411 homo sapien
Q7z411 homo sapien
Q807545 homo sapien
Q80764 rattus norv
Q8can9 mus musculu
P98073 homo sapien
P98073 mus musculu
Q9d319 mus musculu
Q9d319 mus musculu
Q9d312 xenopus lae
Q6nuf5 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obwvc1 homo sapien
Obgr54 xenopus lae
Obdgr1 xenopus lae
ObdevO xenopus tro
O7rty8 homo sapien
Bad18401 homo sapi
O8bik6 mus musculu
O6pf94 mus musculu
OABT9674 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                        Q9dbi0 mus musculu
Q8iu80 homo sapien
Q6uxd8 homo sapien
Aaq88764 homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9y5y6 homo sapien
P56677 mus musculu
Bac35125 mus muscu
Q9jji7 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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3 507.5 13.4 438 507.5 13.4 438 5 507.5 13.4 438 6 506.5 13.4 455 706 13.4 613 706 13.4 719 9 504.5 13.3 558 0 504 13.3 790	4 513.5 13.6 581 5 513 13.5 455 5 513 13.5 471 7 512 13.5 686 8 512 13.5 686 8 512 13.5 686 9 511.5 13.5 448 1 508.5 13.4 445 1 508.5 13.4 445 1 508.5 13.4 445	1 539 14.2 707 2 535.5 14.1 279 2 535.5 13.9 617 4 528.5 13.9 638 5 526.5 13.9 417 7 525.5 13.9 417 7 525.5 13.9 417 7 525.5 13.9 417 7 525.5 13.9 638 6 523.5 13.8 279 8 523.5 13.8 600 0 518 13.7 603 1 518 13.7 603 1 518 13.6 639 3 513.5 13.6 639	500 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	584.5 15.4 701 584.5 15.4 701 584.5 15.4 868 7 584.5 15.3 1134 9 571 15.3 703 577.5 15.2 1524 1 576.5 15.2 1524 2 571 15.1 418 2 571 15.1 418 2 571 15.1 418 3 571 15.1 418 3 571 15.1 418 6 58.5 14.7 492 6 558.5 14.7 492	3 632.5 16.7 680 4 622 16.4 581 5 619.5 16.3 680 6 601 15.9 490 7 601 15.8 490 9 598.5 15.8 490 9 598.5 15.8 490 1 598 15.7 688 2 593 15.7 688
QSYS14 QCZWK6 BACG5495 Q8CDR0 Q8CDR0 Q85T91 Q6DT90 Q86YM4 PLMN_PIG	Q9BYE2 Q9BYE2 Q8CPE0 Q8CPE0 Q6Q1Q9 AAS73179 HATT HUMAN Q7PWE4 Q8CJ17 Q9CJ17	QAGANO QAGANO QAGANO QAJISI TMS3 HUMAN QAJISI QAJISI QAVIKA QAVIKA QAVIKA QAVIKA QATIRX3 QATIR	AAH51839 Q8BM10 Q7ZT70 Q6GPP9 Q6ZND6 BAD18439 Q8ROP5 Q812A6 TMS3 MOUSE TMS3 MOUSE KAL MOUSE Q6ZMG3 AAQ88823 BAD18806 CRYNIA		Q868H7 Q9XZM7 Q9XZM7 Q966H5 Q868H5 Q868H6 Q7TN04 TMS2_MOUSE Q6F7D7 AAH61712 Q920K3 Q868H4 DES1_HUMAN
Qyv514 drosopnila Q6zwk6 homo sapien Bac85495 homo sapien Bac85495 homo sapien Q8cdr0 mus musculu Q03711 xenopus lae Q6dj90 xenopus tro Q86ym4 homo sapien P06867 sus scrofa	homo sap mus musc mus musc gallus g 79 gallus homo sap anophele rattus panuliru	cyprinus rattus r homo sap triakis rattus r mus musc mus musc mus musc mus musc mus musc mus musc rattus r rattus r	homo sampetra musc enopus omo sap homo sap homo sap nusc us musc us musc omo sap homo sap homo sap	nomo sap 76 homo sa rattus r polyandx homo sap rattus r mus musc xenopus rattus r cyprinus homo sap homo sap	branchiost strongyloc strongyloc strongyloc branchiost branchiost mus muscul mus muscul rattus nor rattus nor la rattus nor branchiost homo sapie

ALIGNMENTS

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ST14_HUMAN
ID ST14_H H
AC Q9Y5Y6
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 01-OCT
DT 01-OCT
DT Suppers
DE type s
DE Homo s
OC Eukary
OC Mammal
OX NCBIT
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RT "Rover.
RT "Rever.
RT "Rever.
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RX MEDLIN
RX M
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RY TISSUE=Blood, and Muscle;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Habey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

RA Minting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=99432178; PubMed=10500122;

Takeuchi T., Shuman M.A., Craik C.S.;

"Reverse biochemistry: use of macromolecular protease inhibitors to dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";

"""

Acad. Sci. U.S.A. 96:11054-11061(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ST14 HUMAN STANDARD; PRT; 855 AA. Q9YS'6; Q9BS01; Q9HS05; Q9HS06; Q9HCA3; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Suppressor of tumorisgenicity 14 (EC 3.4.21.-) (Matr type serine protease 1) (MT-SP1) (Prostamin) (Serin (Tumor associated differentially-expressed gene-15 Name=ST14; Synonyms=PRSS14, SNC19, TADG15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=9930381; PubMed=10373424;

Lin C.Y., Anders J., Johnson M., Sang Q.A.,

"Molecular cloning of cDNA for matriptase,

protease with trypsin-like activity.";

J. Biol. Chem. 274:18231-18236(1999).
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"Molecular cloning of a 
in human prostate.";
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                                                                                                                                SEQUENCE
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                                    a novel human serine protease SNC19."; to the EMBL/GenBank/DDBJ databases.
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tase, a matrix-degrading serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigemasa K., Parmley T.H.,
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Pfam; PF00411; CUB; 2.

Pfam; PF00411; CUB; 2.

Pfam; PF00089; Ldl recept a; 4.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CTYMOTRYPSIN.

PRINTS; PR00261; LDLRECEPTOR.

SMART; SM00042; CUB; 2.

SMART; SM00042; LDLa; 4.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01209; LDLRA 1; 2.

PROSITE; PS01209; LDLRA 2; 4.

PROSITE; PS0134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF118224; AAD42765.2; --
EMBL; AF133086; AAF00109.1; --
EMBL; AF030036; BAB20376.1; --
EMBL; AF057145; AAG15395.1; --
EMBL; BC005826; AAH305826.2; --
EMBL; BC003532; AAH30582.1; --
EMBL; AF283256; AAG13949.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                    GG; GO:0005887; C:integral to plasma membrane; TAS. GG; GO:0008236; F:serine-type peptidase activity; TG; GO:0008508; P:proteolysis and peptidolysis; TAS InterPro; IPR000859; CUB.
InterPro; IPR0012172; LDL receptor A. InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001303; Pept_Ser_Cys.
                                                                                                           DOMAIN
DOMAIN
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J. Biol. Chem. 274:18237-18242(1999).
                                                                                                                                                                               Signal-anchor;
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Genew; HGNC:11344; ST14.
MIM; 606797; -.
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Lin C.Y., Anders J., Johnson M., Dickson R.B.;
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                                                                                                                                                                                                      3D-structure; Glycoprotein;
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CUB 1.

CUB 2.

LDL-receptor class A

Charge relay system (

Charge relay system (
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Signal-anchor for type
protein (Potential).
Extracellular (Potentia
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STANDARD;

PRT; 855 AA.

P56677;

15-5UL-1999 (Rel. 38, Created)

16-CCT-2001 (Rel. 40, Last sequence update)

17 16-CUL-2004 (Rel. 44, Last annotation update)

18 Suppressor of tumorigenicity 14 (EC 3.4.21.-) (E

19 Suppressor of tumorigenicity 14 (EC 3.4.21.-) (E

10 Name=St14; Synonyms=Prs814;

11 Nume=St14; Synonyms=Prs814;

12 Nume=St14; Synonyms=Prs814;

13 Nume=St14; Synonyms=Prs814;

24 Nume=St14; Synonyms=Prs814;

25 Mus musculus (Mouse).

26 Eukaryota; Metazoa; Chordata; Craniata; Vertebra

27 Mammalia; Eutheria; Rodentia; Sciurognathi; Muri
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Pred. No. 3.8e-256;
   Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26143132C01F99C9 CRC64;
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      MEROPS; S01.302; -...

MGD; MGI.1338881; St14.

GO; GO:0005576; C:extrinaic to plasma memb
GO; GO:0019897; C:extrinaic to plasma memb
GO; GO:0019897; C:extrine-type peptidase ac
InterPro; IPR001236; F:serine-type peptidase ac
InterPro; IPR0012172; LDL receptor A.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314
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EMBL; BC005496; I
HSSP; P00760; 1E;
MEROPS; S01.302;
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to plasma membrane;

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CHYMOTRYPSIN

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RX MEDLINGE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McEwan R.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,
RA Richards J., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schuzer C.D., Schill J. Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Schmutz J., Myers R.M.,
RA Schuzer G.G., Schill J. S.A., 99:16899-16903(2002).

CC --- SUBCELLULAR LOCARION: Type II membrane protein (Probable).
--- Grand thymus. Not expressed in skeletal muscle, liver, heart, testis
---- Grand thymus. Not expressed in skeletal muscle, liver, heart, testis
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and thymus. Not expressed in skeletal muscle, liver, and brain.
SIMILARITY: Belongs to peptidase family Sl.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 4 LDL-receptor class A domains.
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AAD02230.3; -.
AAH05496.1; -.
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SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRII
                                                                  CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                     SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                       GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                      RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDFCFGQFTCRTGRCIRKELRCD
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                                                                                                                                                                                      GWADCPDYSDERYCRCNATHOFTCKNOFCKPLFWVCDSVNDCGDGSDEEGCSCPAGSFKC
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                                                 CSDGSDEKNCDCGLRSFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLV
                                                                                                                   SNGKCLPQSQKCNGKDNCGDGSDEASCDSVNVVSCTKYTYRCQNGLCLSKGNPECDGKTD
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83.2%;
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Charge relay system (By Charge relay system (By Charge relay system (By N-linked (GlcNAC...)
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Signal-anchor for type I
protein (Potential).
Extracellular (Potential
CUB 1.
CUB 2.
LDL-receptor class A 1.
LDL-receptor class A 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3209; DB 1;
Pred. No. 2.3e-217;
9; Mismatches 56;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630041B06 product:suppression of tumorigenicity 1, carcinoma, full insert sequence.
Mus musculus (Mouse).
Eukaryota; Metaron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Kidney;

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II

"Analysis of the mouse transcriptome based on functional of 170 full-length cDNAs.";

Nature 420:563-573(2002).
                 SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUB=Kidney;
STRAIN=C57BL/6J; TISSUB=Kidney;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Y., Moramatsu M., Hayashizaki Y.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                         Genome
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-21085660; PubMed-11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
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Mammalia; Eutheria;
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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  multicapillary
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[6]
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STRAIN=C57BL/6J; 7
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                                                                                                                                                                                                                                                                                                CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                           GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                                                        QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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                       RNKPGVYTRLPLFRDWIKENTGV
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   RNKPGVYTRLPVVRDWIKEHTGV
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; Pred. No. 2.3e-217;
59; Mismatches 56;
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Q9JJI7;
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MEROPS; S01.302; ---
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:cpptidase activity; IEA.
GO; GO:0006203; F:peptidase activity; IEA.
GO; GO:0006208; P:proteolysis and peptidolysis; IEA.
GO; GO:0006108; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000899; CUB.
InterPro; IPR001172; LDL receptor A.
InterPro; IPR001154; Peptidase_S1A.
InterPro; IPR0011314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00903; Pept Ser_Cys.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF00019; Txypsin; 1.
Pfam; PF00019; Txypsin; 1.
PF00019; Txypsin; 1.
                                                                                                                                                                                                                                                                                             PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PR007261; LDLRECEPTOR.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01209; LDLRA_1; 2.

PROSITE; PS50068; LDLRA_2; 4.

PROSITE; PS50068; LDLRA_2; 4.

PROSITE; PS500134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.
SEQUENCE 855 AA; 94955 MW; 35806B7ECF6CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Wistar; TISSUE-Duodenum; Inoue H., Takahashi K., Kishi K.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: Belongs to peptidase family S1. EMBL; AB037898; BAB03502.1; -. EMBL; AB049189; BAB13765.1; -.
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MEDLINE-21459307; PubMed=11573963;
MEDLINE-21459307; PubMed=11573963;
Satomi S., Yamasaki Y., Tsuzuki S., Hitomi Y., Iwanaga
"A role for membrane-type serine protease (MT-SP1) in j
epithelial turnover.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine protease).
Name=MBSP;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Membrane bound serine protease (Membrane bound ar
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 287:995-1002(2001)
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                                                                                                                                                                                                                                   Local Similarity
hes 567; Conserv
                   181
                                                                                                                                                                     SPYYPGHYPPNIDCTWNIEVPNNQHYKVRFKFFYLLEPRRACGTCFKDYVEINGEKYCGE
                                                                LCGTYPPSYNLTFHSSQNVLLITLITNTERRHDGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                     FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                 LCGTFSPSYNLTFLSSQNVFLVTLITNTDRRHPGFEATFFQLPKMSSCGGLLSEAQGTFS
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Rodentia;
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                                                                                                                                                                                                                                   Score 3197; DB 2;
Pred. No. 1.6e-216;
9; Mismatches 57;
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Sciurognathi; Muridae;
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; Murinae; Rattus.
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                                                          RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., 24 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., 25 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., 26 Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L., 27 Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L., 27 Diatchen M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., 28 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., 28 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., 29 Rahak S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., 29 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., 29 Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., 20 Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., 20 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., 20 Milting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S., 20 Bulkesley R.W., Touchman J.W., Green E.D., Dickson M.C., 21 Bulkesley R.W., Touchman J.W., Green E.D., Dickson M.C., 21 Bulkesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S., 22 Mones S.J., Marra N.A.; Schein J.E., 23 Jones S.J., Marra N.A.; Schein J.E., 24 Jones S.J., Marra N.A.; Schein J.E., 25 Jones C.J., Jones S.J., Marra N.A.; Schein J.E., 25 Jones C.J., Jones S.J., Marra N.A.; Jones S.J., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBWVC1;
01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-MAR-2004 (TrEMBLrel. 26, L
ST14 protein (Fragment).
Name=ST14;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              TISSUE=Colon;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WVC3
                                            Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSQFVVTSNSNKITVRFHSDQSYTDTGFLABYLSYDSSDPCPGQFTCRTGRCIRKELRCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWADCPDYSDERHCRCNATHQFMCKNQFCKPLFWVCDSVNDCGDGSDEEGCSCPAGSFKC
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Last annotation update)
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                 99:16899-16903 (2002)
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05-JUL-2004
05-JUL-2004
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St14-A-prov
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    -!- SIMILARITY: Belongs to peptidase

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                                                                                                                                                                                                                                                                                                                           RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWT
                                                                                                                                                                                                                                                                                                                                                           SDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQ
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                                                                                                                                                                                                                                                                                                              RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWT
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                                                                                                                                            683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.8%; Score 2379; DB 2; 1 larity 100.0%; Pred. No. 2.8e-159; Conservative 0; Mismatches 0;
                                                            PRELIMINARY;
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

27, 27, 27,

Created)

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RX MEDLINE=2238257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley R.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA secnences."
                                          Query
Best I
                                                                                          InterPro; IPRO00859; CUB.
InterPro; IPRO02172; LDL receptor A.
InterPro; IPRO01254; Peptidase SI.
InterPro; IPR001254; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR00903; Pept Ser Cys.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF00457; Ldl recept a; 4.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00122; CUB; 2.
SMART; SM00102; CUB; 2.
SMART; SM00102; CUB; 2.
SMART; SM00102; CUB; 2.
SMART; SM00102; LDLaA 1; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLAA 1; 2.
PROSITE; PS01240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Strausberg R.;
Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
Submitted (MAY-2004) to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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[3]
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                                          y Match
Local
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c. Natl. Acad. Sci. U.S.
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                           393;
                                          Similarity
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                           Conservative
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                                                                                   93593 MW;
                                          60.2%;
57.3%;
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                           125;
                                       Score 2280.5; DB 2; Pred. No. 5.3e-152;
                                                                                   protease.
«; B917386C95BC73BD CRC64;
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                         Mismatches 161;
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                                                      DB 2;
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                     Q9DGR1;
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Homolog of human
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                                                                                                                                                                                                                                                                                                                                    YDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIR
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                                                                                       PRELIMINARY;
 MT-SP1
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                             Name=XMT-SP1;
Xenopus laevis (African clawed frog).
-!- SIMILARITY: Belongs to peptidase
EMBL; AB038498; BAB08218.1; -.
HSSP; P00760; 3BTH.
                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20363741; PubMed=10903452;
                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                    from Xenopus laevis.";
Gene 252:209-216(2000)
                                                                                                                  Yamada K., Takabatake T., Takeshima "Isolation and characterization of
                                                                                                                                             Takeshima K.;
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RR GO; GO:0004295; F:trypsin activity; IEA.
RR GO; GO:0004295; P:proteolysis and peptidolysis; IEA.
RR InterPro; IPR000859; CUB.
RR InterPro; IPR001254; Peptidase_S1.
RR InterPro; IPR001254; Peptidase_S1.
RR InterPro; IPR001314; Peptidase_S1.
RR InterPro; IPR001314; Peptidase_S1A.
RR InterPro; IPR001314; Peptidase_S1A.
RR InterPro; IPR009003; Pept_Ser_Cys.
RR Pfam; PF00057; Ldl recept_a; 4.
RP fam; PF00057; Ldl recept_a; 4.
RR Pfam; PF00059; Trypsin; 1.
RR Pfam; PF00069; Trypsin; 1.
RR Pfam; PF00069; Trypsin; 1.
RR PRINTS; PR00261; LDLBa; 4.
RR PRINTS; PR00261; LDLBa; 4.
RR SMART; SM00042; CUB; 2.
RR SMART; SM000042; CUB; 2.
RR SMART; SM000042; Tryp.SPC; 1.
RR SMART; SM00109; IDLBa; 4.
RR PROSITE; PS01180; CUB; 2.
RR PROSITE; PS01180; CUB; 2.
RR PROSITE; PS01209; LDLBA 1.
RR PROSITE; PS01209; LDLBA 1.
RR PROSITE; PS0134; TRYPSIN_DOM; 1.
RR PROSITE; PS0134; TRYPSIN_DOM; 1.
RR PROSITE; PS0134; TRYPSIN_BIS; UNKNOWN 1.
RR PROSITE; PS0135; TRYPSIN_SER; 1.
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Best Local :
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 I INQTECNKLLDGQLTPRMLCAGFVSGGIDACQGDSGGPLSSVELNNKVYLAGVVSWGEG
                  VINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDG
                                                                                        YDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIR
                                                                                                                                                               WLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFD
                                                                                                                                                                                                                                   DCSDGSDEK--DCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLISPN
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                                                                                                                                                                                                                                                                                                                                                           GWNDCEDFSDEMSCTCTA-LQFRCVNSKLCKPSYFICDGVNDCGDSSDELACKCPNNTFK
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                                                                        NDIAVLELEKPVEYTDFIQPVCIPESTHDFPVGKPIWVTGWGALKEGGGAAVILQKAEIR
                                                                                                                                          MLI SAAHCFQDDHQMRYSDASLWTAYLGLHDQAQLNTKDVVERRIKRIMAHIGFNDNTYD
                                                                                                                                                                                                               DCSDGSDENAAKCNCGKRPFTKKSRIVGGVNADTGEFPWQVSLHAKGNKHTCGASLGFPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           845;
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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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QGDEVO;
QGOT-2004 (TREMBIrel. 28, Created)
Q1-QCT-2004 (TREMBIrel. 28, Last sequence update)
Q1-QCT-2004 (TREMBIrel. 28, Last annotation update)
Q1-QCT-2004 (TREMBIrel. 28, Last annotation update)
Hypothetical protein.
Kenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Strausberg R.; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases EMBL; BC076994; AAH76994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC0769;
Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                       17 KSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                 FHSDQSYTDTGFLAEYLSYDSSDFCFGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSC
                                                                                                                                                       QNVLLITLITNTERRHEGFEATFFQLFRMSSCGGRLRKAQGTFNSFYYFGHYFFNIDCTW
                                                                                                                                                                                                                                               RADAGQMIRLKFKTFKMEKCKANAGDFVMVYDSLSPIEPRAQIRLCGIYPPSYNLTEFSS
                                                                                                                                                                                                                                                                          RGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSS
                                                                                                                                                                                                                                                                                                                                     RAFAVDSLVAYPTDPQIARNFKNSSCAFFLHSSAGVMTKFSSPGFPDTPYPPNARCLWTL
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CARRNKPGVYTKVSMMRDWSKDKTGL
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41.5%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                      91; Mismatches 115;
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SEQUENCE FROM N.A.
MEDLINE-22722134; PubMed=12838346;
Puente X.S., Sanchez L.M., Overall C.M., L
"Human and mouse proteases: a comparative
"human ev. Genet. 4:544-558(2003).
                                                                                                                                                                                             Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamzaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kamchori K., Takahashi-Tujii A., Oshima A., Sugiyama A., Kawakami B., Kanchori K., Takahashi-Tujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Balongs to peptidase family S1.

EMBL; BN000125; CAD67577.1; -.

MEDDE: ARIA 1071; BAD18401.1; -.
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                       EMBL; BN000125; CAD67577.1; -.
EMBL; AK131211; BAD18401.1; -.
MEROPS; S01.072; -.
MEROPS; S01.072; -.
G0; G0:0016021; C:integral to membrane; IEA.
G0; G0:0004263; F:chymotrypsin activity; IEA.
G0; G0:0004295; F:trypsin activity; IEA.
G0; G0:0004295; F:trypsin activity; IEA.
G0; G0:0004295; F:trypsin activity; IEA.
G0; G0:0006508; P:proteolysis and peptidolysis;
InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Catarrhini; Hominidae;
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Pfam; PF000431; CUB; 1.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00726; LDLRECEPTOR.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01109; LDLRA 1; 1.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HE; UNKN

PROSITE; PS00135; TRYPSIN HE; UNKN

PROSITE; PS00135; TRYPSIN HE; UNKN

PROSITE; PS00135; TRYPSIN HE; UNKN

PROSITE; PS00136; 
     BAD18401;
BAD18401;
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                                                                                                                                                                                                                                                          DGCAQRNKPGVYTRLPLFRDWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRVPSPLVHIQLQCSSRLSDKPLLAEYGSYNISQPCPVGSFRCSSGLCVPQAQRCDGVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTSNSNKITVRFHSDQSYTDTGFLABYLSYDSSDPCP-GQFTCRTGRCIRKELRCDGWAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPPKCKCTWKFQT-SLSTLGIALKFYNYSITKKSMKGCEHGWWEINBHMYCGSYMDHQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE--RSQFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFVSTNNLMLVTFKSPHIRRLSGIRAYFEVIPEQKCENTVLVKDITGFEGKISSPYYPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHFKLVAIVGYLIRLSIKSIQI-EADNCVTDSLTIYDSLTPIRSSILYRIC--EPTRTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVOLCGTYPPSYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTDHSDELNCSCDAGHQFTCKNKFC---KPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease;
     (TrEMBLrel.
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                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64041 MW;
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Peptidase_S1A.
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                                                                                                                                                                                                                                                                                                              -GIITSRMLCAGIMSGKRDACKGDSGGPLSCRRKSDGKWILTGIVSWG
     27,
27,
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       Last sequence update)
                            Created)
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Pred. No. 2.86
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type II transmembrane serine; 0458CBEA996EA285 CRC64;
                                                                                 PRT;
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?.8e-63;
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SORET RAPARA

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R EMBL; AKI31211; BAD18401.1; -.

Q SEQUENCE 572 AA; 64041 MW; 0458CBEA996EA285 CRC64;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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CDNA FLJ16088 fis, clone NT2RP7008435, weakly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4.21.-
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                                                                                                                                                                                                                                                                                          IALLELE--KPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHT-QYGGTGALILQKGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                        PDGSDEEGCTCS-RSSSALHRIIGGTDTLEGGWPWQVSLHFVGSAY-CGASVISREWLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP-GQFTCRTGRCIRKELRCDGWAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE--RSQFV
                                                                                                                                    DGCAQRNKPGVYTRLPLFRDWI
                                                                                                                                                                                                       RVINQTTCENLLEQQITPRMMCVGFLSGGVDSCQGDSGGPLS-SVEADGRIFQAGVVSWG
                                                                                                                                                                                                                                                                                                                                                                                    AAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS--APGVQERRLKRIISHPFFNDFTFDYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGPLI ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFVSTNNLMLVTFKSPHIRRLSGIRAYFEVIPEQKCENTVLVKDITGFEGKISSPYYPSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHFKLVAIVGYLIRLSIKSIQI-BADNCVTDSLTIYDSLLPIRSSILYRIC--EPTRTLM
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                                                                                            HGCGRPNFPGVYTRVSNFVPWI
                                                                                                                                                                               ELIDQTLCVSTY-GIITSRMLCAGIMSGKRDACKGDSGGPLSCRRKSDGKWILTGIVSWG
                                                                                                                                                                                                                                                                  IALLQLSIAWPETLKQL1QPICIPPTGQRVRSGEKCWVTGWGRRHEADNKGSLVLQQAEV
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1017.5;
Pred. No. 2.8e
98; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                      677
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2.8e-63;
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                                                                                                                                                                                                                                                                                                                                                   -VRRIVVHEYYNSQTFDYD
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Isogai T.;
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        SEQUENCE FROM N.A.

(CSTRAIN=C579EL/61) TISUB=Corpora quadrigemina;

(CSTRAIN=C579EL/61) TISUB=Corpora quadrigemina;

(A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., A Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,

(A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume T.,

(A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

(A Hayashida K., Hayatsu N., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

(A Hori F., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S.,

(A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

(A Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

(A Kurihara C., Mateuyama T., Mumazaki R., Ohno M., Ohsato N., Okazaki Y.,

(A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

(A Sasaki D., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

(A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogahe Y., Tanaka T.,

(A Sasaki D., Takahashi F., Takaka-Akahira S., Takeda Y., Tanaka T.,

(A Tomaru A., Toya T., Yasunishi A., Muzamatsu M., Hayashizaki Y.;

(L Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, 1
enriched library, clone:B230219123 product:weakly si
COAGULATION FACTOR XI.
Name-B23021972351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-Corpora quadrigemina;
MEDLINB-20530913, PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Iknjani T., Kashiwagi K.,
Yamamoto R., Matsumoto H., Sakaguchi N., Kegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA), system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare full-length cDNA librar Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE=Corpora quadrigemina;

MEDLINE=20499374; PubMed=11042159;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibatkonno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Corpora qu
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=B230219I23Rik;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303:19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quadrigemina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00042; CUB; 1.

SMART; SM000192; LDLA; 3.

SMART; SM00020; Tryp_SPC; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS01209; LDLRA 2; 2.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.

Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; pF000431; CUB; 1.
pfam; pF000631; Ldl_recpt_a; 3.
pfam; pF00069; Trypsin; 1.
pRINTS; pR00722; CHYMOTRYPSIN.
pRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
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HSSP; P00760; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.072; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0004263; F:chymotrypsin activity; IEA.
GO:0004295; F:trypsin activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to peptidase family S1. L; AK045663; BAC32448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:2686594; B230219I23Rik.
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                                                                                                                                                                                                                                                                    364
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                            599
                                                                                                                   375
                                                                                                                                                 484
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                                                         426
 486
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                                                                                                                                      HCYIDDRGFRYSDPTQWTAFLGLHDQSQRS--APGVQERRLKRIISHPFFNDFTFDYDIA
                                                                                                                                                                                           GSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPPNIDCTWNIEUPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE--RSQF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNL 131
                                                                                                                                                                                                                                       PLV-----CDGFRDCEDGQDEQNCTR--SIPCTSRTFKCGNDICFRKQNAQCDGIVDCPD
                                                                                                                                                                                                                                                                    KCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSD
                                                                                                                                                                                                                                                                                                                                                          IFRVPSPLVHIQLQCSSRLSDKPLLVEYGGYNISQQCPAGSFRCSSGLCVPQAQRCDGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHFKLVAIVGYLIRLSIESIQL-EADNCITDSLTVYDSLLPIRSAILYRIC--EPTRTLM
                                                                         LLELE--KPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHT-QYGGTGALILQKGEIRV
                                                                                                                                                                          GSDEEGCGCS-RSSSFLHRIVGGSDSQEGTWPWQVSLHFVGSAY-CGASVISREWLLSAA
                                                                                                                                                                                                                                                                                                  DCFDESDELFCVT------VKP------ACNSSSFR-QHG
                                                                                                                                                                                                                                                                                                                             DCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNG
                                                                                                                                                                                                                                                                                                                                                                                        VVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP-GQFTCRTGRCIRKELRCDGWA 303
                                                                                                                                                                                                                                                                                                                                                                                                                       YYPPKCKCTWTFQT-SLSTLGIALKFYNYSITKKSAKGCEHGWWEINEHMYCGSYMDHET 176
 IDQTVCVSTY-GIITSRMLCAGVMSGKSDACKGDSGGPLSCRRKSDGKWILTGIVSWGHG
                            INQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLS-SVEADGRIFQAGVVSWGDG
                                                         LLQLSIAWPETLKQLIQPICIPPAGQKVRSGEKCWVTGWGRRHEADSKGSPVLQQAEVEL
                                                                                                                  HCF---HGNRLSDPTPWTAHLGMYVQGNAKFISP-----VRRIVVHEYYNSQTFDYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; Serine pi
572 AA; 63757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.8%; Score 1015.5; DB 36.3%; Pred. No. 3.9e-63; tive 98; Mismatches 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease.
N; 21C0EC523B5F4301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572;
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544
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RESULT
Q6PF94
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RX MEDLINE-22380257; PubMed=12477932;

RX MEDLINE-22380257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Racha S.S., Loquellano N.A., Peters G.J., Abramoon R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RA Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Jones J., Wall J., Wall
Query Match
Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- SIMILARITY: Belongs to peptidase fami.

EMBL; BC057674; AAH57674.1; -.

GO; GO:0005886; C:plasma membrane; IDA.

InterPro; IPR000859; CUB.

InterPro; IPR001272; LDL receptor A.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR009303; Pept Ser Cys.

Pfam; PF00057; Ldl recept a; 2.

Pfam; PF00089; Trypsin; 1.
                                                                                                                                                                                                SMART; SM00192; LDLa; 3.
SMART; SM00192; Tryp Sec; 1.
PROSITE; PS01105; CUB; 1.
PROSITE; PS01109; LDLRA 1; 1.
PROSITE; PS01209; LDLRA 2; 3.
PROSITE; PS50240; TRYPSIN DOM; 1
PROSITE; PS00134; TRYPSIN HIS; UD
PROSITE; PS00135; TRYPSIN SER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6PF94;
                                                                                                                                    Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Impres6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg
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STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAQRNKPGVYTRLPLFRDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SEP-2003) to the EMBL/GenBank/DDBJ databases NRITY: Belongs to peptidase family S1.
                                                                                                                                    Protease;
799 AA;
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; Rodentia;
                                                                                                                                    89557 MW
                                  26.8%;
   3%; Score 1014; D
1%; Pred. No. 7.2e
107; Mismatches
                                                                                                                                        MW.
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Last sequence update)
Last annotation updat
                                                                                                                                    protease.
W; 16315A646A4D5288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677
                                                                                                                                                                                                                               UNKNOWN_1.
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   ; DB 2;
7.2e-63;
hes 233;
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                                                                                                                                        CRC64;
                                                                  Length 799;
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Conservative

Indels

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Gaps

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02-MAR-2004
02-MAR-2004
MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C. Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Mrange C. Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Mallahy Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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STRAIN=FVB/N; TISSUE=Liver;
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Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield N.Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.
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NCE 799 AA; 89557 MW; 16315A646A4D5288
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777 660 657

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RC STRAIN-ECSTBL/G; TISSUB-Liver;
RX MEDLINE-22354683; PubMed-1246685; DOI=10.1038/nature01266;
RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Gassterland T., Gariboldi M., Cissi C., Godzik A., Gough J.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglatt D.R., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravsai T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravsai T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                      XX SEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XX Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
XX Altapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Altapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altapleton M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,
XX Altapleton M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
XX Altapleton M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
XX Altapleton M.J., Watteman M., Madan A., Rodrigues S., Sanchez A.,
XX Altapleton M.J., Watteman M., Madan A., Rodrigues S., Sanchez A.,
XX Altapleton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Altapleton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Altapleton M.J., Watteman M.J., Watten B.D., Dickson M.C.,
XX Altapleton M.J., Watten B.D
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Nature
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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420:563-573(2002).
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse hepsin in adult and embryonic
99:16899-16903 (2002)
                                                                                                     of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              based on functional annotation
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R MGD; MGI:1919003; Impres6.

R GG; GO:0016021; C:integral to membrane; ISS.

R GG; GO:0005886; C:plasma membrane; IDA.

R GG; GO:0005886; C:plasma membrane; IDA.

R GG; GO:0004252; F:serine-type endopeptidase activity; ISS.

R GG; GO:0001525; F:angiogenesis; ISS.

R GG; GO:0030198; P:extracellular matrix organization and bioge

R GG; GO:0030198; P:extracellular signaling cascade; ISS.

R GG; GO:00042730; F:intracellular signaling cascade; ISS.

R GG; GO:0004278; F:intracellular signaling cascade; ISS.

R GG; GO:0006508; P:proteolysis and peptidolysis; ISS.

R InterPro; IPR000859; CUB.

R InterPro; IPR001274; LDL receptor A.

R InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0761; LDLRECEFOR.
PROSITE; PS001180; CUB; 1
PROSITE; PS01209; LDLRA 1; 1.
PROSITE; PS50068; LDLRA 2; 3.
PROSITE; PS50040; TRYPSIN DOM; 1
PROSITE; PS50240; TRYPSIN HIS; 1
PROSITE; PS00134; TRYPSIN HIS; 1
PROSITE; PS00135; TRYPSIN HIS; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Metastasis Rev. 22:237-258(2003).

-!- FUNCTION: May play a specialized role in processes in liver (By similarity).

-!- SUBCELLULAR LOCATION: Type II membrane px
-!- TISSUE SPECIFICITY: Expressed at highest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bugge T.H., Antalis T.M.;

"Membrane anchored serine proteases: a rapidly expanding surface proteolytic enzymes with potential roles in cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [4]
REVIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22668120; PubMed=12784999;
                                                                                                                                                                                               Glycoprotein;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00760;
                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the nasal cavity and pharyngo-tympanic tubes. SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 CUB domains. SIMILARITY: Contains 3 LDL-receptor class A domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: Expressed at higher levels from 12.5 15.5 dpc with a peak at 13.5 dpc. Expression in the devel liver as well as a restricted set of embrionic epithelial
                                                                                                                                                                                                                                                                                                                                        PF00057; Ldl_recept_a; 2.
PF00089; Trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY240929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK004939;
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      213
323
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323
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AAH29645.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            P:extracellular matrix organization and bioge.
P:fibrinolysis; ISS.
P:intracellular signaling cascade; ISS.
P:proteolysis and peptidolysis; ISS.
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      811
336
440
477
514
555
799
617
668
                                                                                                                                                                  80
                                                                                                                                                                                                           Repeat;
   protein (Potential).
Extracellular (Poten CUB 1.
CUB 2.
LDL-receptor class A
LDL-receptor class A
LDL-receptor class A
Charge relay system
Charge relay system
                                                                                                                                                                  Signal-anchor
                                                                                                                                                                                Cytoplasmic
                                                                                                                                                                                                             Serine protease; Signal-anchor;
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      system system system
                                                                                                                                                                                (Potential)
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st levels
                                                                                                                                       (Potential)
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      УВ)
УВ)
                                                               ω N P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer.";
       similarity), similarity), similarity), similarity),
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Best Local Sim:
Matches 213;
                                                                                                                              TMS6_HUMAN
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CARBOHYD
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CONFLICT
           HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606.
                                                                               Q8IUBO; Q8IUE2; Q8IXV8;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                        Transmembrane protease, serine Name=TMPRSS6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                           541
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                                                                                                                                                                                                    RNKPGVYTRLPLFRDWIKE
                                                                                                                                                                                                                                                                                                                                                                                              CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNFFGVYTRVTRVINWIQQ
                                                                                                                                                                                                                                      QDLCSEAYRYQVSPRMLCAGYRKGKKDACQGDSGGPLVCREPSGRWFLAGLVSWGLGCGR
                                                                                                                                                                                                                                                                                                          ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                                                                                                          SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                                                                                                                CRDGSDEQHCDCGLQGLS--SRIVGGTVSSEGEWPWQASLQIRGR-HICGGALIADRWVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WADCTDHSDELNCSCDAGHOFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGER-----
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                                                                                                                                                                                                                                                            QTTCENLLPQQTTPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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Pred. No. 7
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P -> PP (
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N-linked
N-linked
N-linked
N-linked
N-linked
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                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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32EB3E7C3127801B
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                                                                   n update)
3.4.21.-)
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7.3e-63;
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                                                                    (Matriptase-2).
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RH HODDEN J.D. (011997 J.P.)

RH HODDEN J.D. (011997 J.P.)

RH TYPRESS6, a new type II cransmembrane serine protease.*;

RH STORMER J.D. (011997 J.P.)

RE SHOUTHER COSTINGS PROM N.A.

RE SHOUTHER J.D. (011997 J.P.)

RE SHO
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Pfam; PF00431; CUB; 1.

Pfam; PF0069; Ldl recept a; 2.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR0072; CHYMOTRYPSIN.

PRINTS; PR0072; CUB; 1.

SMART; SM00042; LDLa; 3.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS0120; LDLRA 1; 1.

PROSITE; PS0120; LDLRA 2; 3.

PROSITE; PS00240; TRYPSIN DOM; 1.

PROSITE; PS0034; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in human liver and showing degrading activity against extracellular matrix proteins."; J. Biol. Chem. 277:37637-37646(2002).
                                                                                                                                                                                                                                                                                         InterPro; IPR002172; LDL receptor A. InterPro; IPR001254; Peptidase S1. InterPro; IPR001314; Peptidase S1A. InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ319876; CAC85953.1; ALT_INIT. EMBL; AY055383; AAL16413.1; -.
DOMAIN
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"Membrane anchored serine proteases: a rapidly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22668120;
Netzel-Arnett S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22241917; PubMed=12149247; DOI=10.1074/jbc.M203007200; Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.; "Matriptase-2, a membrane-bound mosaic serine proteinase predo
                          Serine protease;
DOMAIN 1
TRANSMEM 56
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TISSUE=Fetal
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SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 3 LDL-receptor class A domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2
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AL022314; -; NOT ANNOTATED CDS.
BC039082; AAH39082.1; -.
P00760; 1EZX.
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                                                                        splicing; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                        :16517; TMPRSS6.
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 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          experimental
                                                         Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12784999;
Hooper J.D., Szabo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 99:16899-16903(2002)
 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_008379,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ence=VSP_008379, VSP_008380; confirmation available;
Cytoplasmic (Potential).
Signal-anchor for type II
protein (Potential).
Extracellular (Potential).
                                                          Transmembrane.
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                                                                        Repeat;
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                                                                                                                                 RLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGH
                                                                                                                                                                             QVRGR-HICGGALIADRWVITAAHCFQED---
                                                                                                                                                                                              HALGOGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQER
                                                                                                                                                                                                                                    DNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLALWFDAYALRRQKYDLPCTQGQ
   ALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQ
                             EADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE
                                                          LREGGPISNALQKVDVQLIPQDLCSEVYRYQVTPRWLCAGYRKGKKDACQGDSGGPLVCK
                                                                                   TOYGGTGALILOKGEIRVINOTTCENLLPOOITPRIMCVGFLSGGVDSCQGDSGGFLSSV
                                                                                                                   KVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPARSHFFEPGLHCWITGWGA
                                                                                                                                                                                                                                                                   RCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSL
                                                                                                                                                                                                                                                                                                 CPNGLDERNCVCRA-TFQCKEDSTCISLPKVCDGQPDCLNGSDEEQCQE--GVPCGTFTF
                                                                                                                                                                                                                                                                                                                CGDNSDEQGCSCPAQTFRC-SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTY
                                                                                                                                                                                                                                                                                                                                                           PGEFLCSV--
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811 AA;
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34.0%;
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Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlcNAc. . .) (Potential).
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CUB 2.
LDL-receptor class /
LDL-receptor class /
LDL-receptor class /
Serine protease.
Charge relay system
Charge (GleNAc...
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/FTId=VSP_008380.
/FTId=VSP_008380.
A -> V (in Ref. 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1007; DB 1;
Pred. No. 2.3e-62;
9; Mismatches 229;
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                                                                                                                                                                                -SMASTVLWTVFLGKVWQNSR-WPGEVSF
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Best Local Similarity
Matches 217; Conserv
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SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=22887296; PubMed=12975309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=UNQ354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY358398; AAQ88764.1;
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"The secreted protein discovery initiative (SPDI), a rarys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6UXD8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00089; Trypsin; 1.
S; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00431; CUB; 1.
PF00057; Ldl_recept_a; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
WTIQNRRLCGLRILQPYAERIPVVATAG--
                                                               VEINGEKYCG----
                                                                                                                               DNRLDSQGVLSTPYEPSYYSPQTHCSWHLTVPSLDYGLALWFDAYALRRQKYDLPCTQGQ
                                                                                                                                                                                                       GRIRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDY
                                                                                                                                                                                                                                                                                      SRQEPVVEVLASGAIMAVVWKKGLHSYYDPFVLSV----
                                                                                                                                                                                                                                                                                                                                                          GTYPPSYNLT-----FHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCG
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(Taroa; Chordata;
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34.0%;
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W; 8726C91B1E02E163 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1005; DB 2;
Pred. No. 3.1e-62;
8; Mismatches 230;
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02-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                      Genome
EMBL; A
                                                                                                                                                                                                                                                                                                                                                                       Effort to Identify Novel Human Secreted and Bioinformatics Assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                   AY358398; AAQ88764.1;
                                                                                                                                                                                                                                            Similarity
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SROEPVVEVLASGAIMAVVWKKGLHSYYDPFVLSV
                                                       GTYPPSYNLT-----
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                                                                                                         PDHLASSCLWHLQGPKDLMLKLRL-EWTLAECRDR----LAMYDVAGPLEKRLITSVYGC
                                                                                                                                                           PAH--ARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQL--C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LREGGPISNALOKVDVQLIPODLCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QCEDRSCVKKPNPQCDGRPDCRDGSDEEHCDCGLQG--PSSRIVGGAVSSEGEWPWQASL
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                          88845 MW; 8726C91B1E02E163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primata;
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                                                                                                                                                                                                                                         26.5%;
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Last annotation update)
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                                                                                                                                                                                                                                         Score 1005; DB 2;
Pred. No. 3.1e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                Indels
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     QPVVFQACEVNLTL
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DR REAL SECONDRICATION OF THE PROPERTY OF THE 
  Pfam; PF00431; CUB; 1. F---
Pfam; PF00087; Ldl recept_a; 2.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR007261; LDLRECEPTOR.
SMART; SM00192; LDLa; 3.
SMART; SM00192; LDLa; 3.
SMART; SM00192; LDLa; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01209; LDLRA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OGICC2 PRELIMINARY;
OGICC2;
O5-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
DJ1170X4.2 protein.
                                                                                                                                                                                InterPro; IPR000859; CUB.
InterPro; IPR0022172; LDL receptor A.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                    Beare D.M., Dunham I.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; CR456446; CAG30332.1;
                                                                                                                                                                                                                                                                                                                                                                       Collins J.E., Wright C.L., Edwards Cole C.G., Goward M.E., Aguado B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=dJ1170K4.2;
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Last annotation update)
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Catarrhini; Hominidae; Homo.
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Mallya M., Mokrab
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) Y., Huckle
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-1е Е.J.,
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      CAG30332
ID CAG30332
AC CAG30332;
AC CAG30332;
AC O1-JUN-200
DT 01-JUN-200
DT 01-JUN-200
DT 01170K4.2
GN DJ1170K4.2
GN DJ1170K4.2
GN DJ1170K4.2
OS Homo Bapie
OC Eukaryota;
OX NCBI_TaxID
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Best Local S
Matches 217
01-JUN-2004 (TrEMBLrel. 2
01-JUN-2004 (TrEMBLrel. 2
01-JUN-2004 (TrEMBLrel. 2
01170K4.2 protein.
DJ1170K4.2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Prima
NCBI_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0068; LDLRA_2; 3.
PROSITE; PSS0240; TRYPSIN_DOM; 1
PROSITE; PS00134; TRYPSIN_SER; 1
PROSITE; PS00135; TRYPSIN_SER; 1
Hydrolase; Protease; Serine prot
SEQUENCE 824 AA; 91333 MW; A
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217; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPNGLDERNCYCRA-TFQCKEDSTCISLPKYCDGQPDCLNGSDEEQCQE--GVPCGTFTF
                                                                                                                                                                                                                                                                                                                                                                                                   AGYRKÓKKDACÓGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVÝTRITGVISWIQ
                                                                                                                                                                                                                                                                                                                                                                                                                      VGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGDNSDEQGCSCPAQTFRC-SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTIQNRRLCGLRILQPYAERIPVVATAG---ITINFTSQISLTGPGVRVHYGLYNQSDPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRQEPVVEVLASGAIMAVVWKKGLHSYYDPFVLSV-----QPVVFQACEVNLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTYPPSYNLT------FHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAH--ARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQL--C
                                                                                                                                                                                                                                                                                                                                                             679
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                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Serine protease 91333 MW; A74F1
                                              Chordata;
                             Primates;
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Pred. No. 8.2e-61
98; Mismatches 23
                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A74F186406041F7B CRC64;
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                                                                                                                               sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LILQKGBIRVINQTTCENLLPQQITPRMMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SMASTVLWTVFLGKVWQNSR-WPGEVSF
                                                                                                                                                                                                                ₿
                                                                                                                               update)
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Best Local (
                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Enteropeptidase precursor (EC 3.4.21.9) (Enteropeptidase precursor)
Name=PRSS7; Synonyms=ENTK;
Sus scrofa (Pig)
                                                                                                                                                          ENTK PIG
P98074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
COLING J.E., Wright C.L., Edwards C.A., Davis M.P., Gri.
Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y.,
Beare D.M., Dunham I.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR456446; CR4303331; -. R74F186406041F7B CRC64;
       Sus scrofa 
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPARSHFFEFGLHCWIIGWGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAPGVQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCEDRSCVKKPNPQCDGRPDCRDGSDEEHCDCGLQG--PSSRIVGGAVSSEGEWPWQASL
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       Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              824 AA;
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                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%;
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    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A74F186406041F7B CRC64;
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Mokrab Y., Huc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NGLCVP---ACDGVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huckle
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       InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR0002172 AAM.
InterPro; IPR0001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001013; Pept S1A enterop.
InterPro; IPR0009003; Pept Ser_Cys.
InterPro; IPR000082; SEA.
InterPro; IPR001190; Sror_receptor.
                                                                                                                                                                                                                                                                   Pfam; PF01390; SEA; 1.
Pfam; PF000530; SRCR; 1.
Pfam; PF000089; Trypsin; 1.
PIRSF; PIRSF001138; Enteropeptidase; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLEECEPTOR.
PRINTS; PR00261; LDLEECEPTOR.
PRINTS; PR00260; MANDOMAIN.
SMART; SM00202; SR; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; P801180; CUB; 2.

PROSITE; P801209; LDLRA_1; 2.

PROSITE; P850068; LDLRA_2; 2.

PROSITE; P8500740; MAM_1; 1.

PROSITE; P8500740; MAM_2; 1.

PROSITE; P850060; MAM_2; 1.
                                                                                                                                                                               SMART; SM00042; C
SMART; SM00192; I
SMART; SM00137; N
SMART; SM00200; S
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Matsushima M., Ichinose M., Yahagi N., Kakei N., Tsukada S., Miki K.,
Kurokawa K., Tashiro K., Shinokawa K., Shinomiya K., Umeyama H.,
Inoue H., Takahashi T., Takahashi K.;
"Structural characterization of porcine enteropeptidase.";
J. Biol. Chem. 269:19976-19982(1994).
J. Biol. Chem. 269:19976-19982(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Duodenal mucosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleaved by a trypsin-like protease.

PTM: The mini chain may be cleaved by elastase.

SIMILARITY: Belongs to peptidase family S1.

SIMILARITY: Contains 2 CUB domains.

SIMILARITY: Contains 2 LDL-receptor class A dom

SIMILARITY: Contains 1 MAM domain.

SIMILARITY: Contains 1 SEA domain.

SIMILARITY: Contains 1 SECR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type II membrane protein (Probable) PTM: The chains are derived from a single precursor that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (heavy) chain, and a mini chain. SUBCELLULAR LOCATION: Type II me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trypsinogen.
SUBUNIT: Het
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00431;
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; Ldl_recept_a;
; MAM; 1.
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                                                                                                                                                        CUB; 2.
LDLa; 2
MAM; 1.
SEA; 1.
SR; 1.
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Peptidase_S1A.
Pept_S1A_enterop.
Pept_Ser_Cys.
SEA.
SEA.
STOT_receptor.
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Similarity 32.4%;
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PS50287;
PS50240;
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  RRACGTCPKDYVEI-NGEK------
                                                            QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP
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                                           ELP--TDCGGPFELWEPNTTFTSMNFPNNYPNQAFCVWNLNAQKGKNIQLHFEEFDLEN-
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10; TRYPSIN DOW; 1.
34; TRYPSIN HIS; 1.
35; TRYPSIN SER; 1.
sequencing; Glycoprotein; Hydrolase; Lipoprotein; sequencing; Glycoprotein; Hydrolase; Transmembrane;
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                                                                                                                                                                  By similaril N-linked (G. N-lin
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CUB 2.
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Charge
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Signal-anchor for type II
protein (Potential).
Extracellular (Potential).
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Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
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01-MAR-2004 (TrEMBLrel.
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MEROPS; S01.358; --
MEROPS; S01.969; --
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PNRPGVYARVPKFTEWIQ 1030
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    protease.
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GSDEKDCDCGLRSFTRQA--RVVGGTDADEGEWPWQVSLHALGQGH1CGASL1SPNWLVS
EKCQQQMPEYNITENMMCAGYEEGGIDSCQGDSGGPLMCLE-NNRWLLAGVTSFGYQCAL
                                              TTCENLLPQ-QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                     MMHLEFKVNYTDYIQPICLPEENQVFPPGRICSIAGWGKVIYQGSPADILQEADVPLLSN
                                                                                                                                                            LIELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQ
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G); GO:0004295; F:trypsin activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR002154; Peptidase S1.
Pfam; PP00057; Ldl_recept_a; 1.
Pfam; PP00057; Ldl_recept_a; 1.
Pfam; PP00059; Trypsin; 2.
Pfam; PF00059; Trypsin; 2.
SMART; SM00192; LDLa; 1.
SMART; SM00192; Tryp_SPC; 2.
PROSITE; PS50068; LDLA; 2; 1.
PROSITE; PS50068; LDLA; 2; 1.
PROSITE; PS500134; TRYPSIN_HIS; UNKNOWN_2.
PROSITE; PS500134; TRYPSIN_HIS; UNKNOWN_2.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_2. MEDLINE=22784742; PubMed=12886014; Created) Last seq Last ann 100:9185-9190(2003). Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. PRT; sequence update) annotation updat with 855 the ability to a single transl B update) generate

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GO; GO:0006508; P:proteolysis and peptidolysis; IE.
GO; GO:0006508; P:proteolysis and peptidolysis; IE.
InterPro; IPR002172; LDL receptor A.
InterPro; IPR001254; Peptidase S1.
Pfam; PP00057; Ldl recept a; 1.
Pfam; PP00089; Trypsin; 3.
SMART; SM00192; LDLa; 1.
SMART; SM00192; LDLa; 1.
SMART; SM001020; Tryp SPC; 3.
PROSITE; PS50068; LDLRA 2; 1.
PROSITE; PS50068; LDLRA 2; 1.
PROSITE; PS500134; TRYPSIN DOM; 3.
PROSITE; PS500134; TRYPSIN JER; 2.
PROSITE; PS00135; TRYPSIN JER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ488946; CAD35758.1; -
MEROPS; S01.357; -.
MEROPS; S01.358; -.
MEROPS; S01.758; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7Z411
Q7Z411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  product."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                          Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Polyserase-I, a human polyprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22784742; PubMed=12886014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyserase-IA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132;
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
CTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQA-RVVGGTDADEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQA-RVVGGTDADEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGPLVCEEPSGRFFLAGIVSWGIGCAEARRPGVYARVTRLRDWILEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WVTGWGHTQYGG-TGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASTVR-AQVVQIVKHPLYNADTADFDVAVLELTSPLPFGRHIQPVCLPAATHIFPPSKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FPWQASLRE-NKEHFCGAAIINARWLVSAAHCFNE----FQDPTKWVAYVGATYLSGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPGNSFSCGNSQCVTKVNPECDDQEDCSDGSDEAHCECGLQPAWRMAGRIVGGMEASPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 25, 1) (TrEMBLrel. 25, 1) (TrEMBLrel. 26,
                                                                                                                        Protease;
1059 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                      18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91352 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.9%;
45.7%;
                                                                                                                        Serine protease.
114020 MW; 17D27A2D99F2A264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    S.A.
                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 717.5;
Pred. No. 5.8e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence up
Last annotation
                                                     Score 717.5; DB 2;
Pred. No. 7.3e-42;
3; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                    100:9185-9190(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8AF2759D9740CF3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.8e-42;
95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the ability to a single transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                                                 IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation
                                                      Indels
                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Homo.
                                                                                      1059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435
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                                                      9
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632
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 RESULT 23

ENTK_BOVIN

ID ENTK BOVIN

AC P98072;
DT 01-FEB-1996
RC TISSUE-Duode
RX MEDLINE=943
RA Kitamoto Y.
RY "BITCHEROKINAS
RT "BITCHEROKINAS
RT "BITCHEROKINAS
RT "BITCHEROKINAS
RT "Cloning and to f. k.
[2]
RP SEQUENCE OF
RX MEDLINE=940
RA LAVALLE E.H.
RA GRANT K.L.
RT "Cloning and to f. k.
RI [3]
DFOCEONING OF
RX MEDLINE=91146
RT "CLONING OF
RX MEDLINE=9116
RT "THE amino-t
RT SUBUNIT OF k.
RA Light A.
J. Protein of
CC -i- FUNCTION
CC -i- FUNCTION
CC -i- SUBUNIT
CC -i- SUBUNIT
CC -i- SUBUNIT
CC -i- SUBCELLI
CC LEVENTE-NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94043122; PubMed=8226855;
Lavallie E.R., Rehemtulla A., Rac
Grant K.L., Light A., McCoy J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                             J. Protein Chem. 10:475-480(1991)
                                                                                                                                                                                                                                                                                               enterokinase.";
                                                                                                                                                                                                                                                                                                                             MEDLINE=92189715; PubMed=1799406;
Light A., Janska H.;
                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and functional expression of a subunit of bovine enterokinase.";
J. Biol. Chem. 268:23311-23317(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 801-1035 FROM N.A.,
                                                                                                                                                                                                                                                                                                               "The amino-terminal
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Intestine;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 801-827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovinae; Bos
                                                                                     multidomain (heavy) chain link
SUBCELLULAR LOCATION: Type II
ALTERNATIVE PRODUCTS:
                                                                                                                      SUBUNIT: Heterodimer of a catalytic multidomain (heavy) chain linked by
                 Name=Short
                                                     Name=Long
                                                                        Event=Alternative
                                                                                                                                                        trypsinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
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     IsoId=P98072-2;
                                     IsoId=P98072-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPGNSFSCGNSQCVTKVNPECDDQEDCSDGSDEAHCECGLQPAWRMAGRIVGGMEASPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND PARTIAL
 Sequence=VSP_005386
                                     Sequence=Displayed;
                                                                     splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Racie L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1035
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p99072;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Enteropeptidase precursor (EC 3.4.21.9) (Ente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94329561; PubMed=8052624;
Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E
"Enterokinase, the initiator of intestinal digestion,
protease composed of a distinctive assortment of doma
Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
                                                                                                                                     FUNCTION: Responsible for initiating activation of pancreatic proteolytic procenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases.

CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGGPLVCEEPSGRFFLAGIVSWGIGCAEARRPGVYARVTRLRDWILEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wvrgwghrqygg-rgalilokgeirvingrrcentlpggirprwwcvgflsggvpscogb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASTVR-AQVVQIVKHPLYNADTADFDVAVLELTSPLPFGRHIQPVCLPAATHIFPPSKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPWQASLRE-NKEHFCGAAIINARWLVSAAHCFNE----FQDPTKWVAYVGATYLSGSE
                                                                                                                                                                                                                                                                                                                                        sequence of the catalytic subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Eute Cetartiodactyla; Ruminantia; Pecora;
Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND PARTIAL
                                          membrane
                                                                 (light) chai
a disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Enterokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diblasio
                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding
                                                                                             chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
cora; Bovidae;
                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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                                                                                                                                                                                                                                                                                                                                          bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mosaic
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MEROPS; S01.156;
InterPro; IPR000859; CUB.
InterPro; IPR0002172; LDL receptor_A.
InterPro; IPR0002172; LDL receptor_A.
InterPro; IPR0002154; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001313; Pept_S1A enterop.
InterPro; IPR00103; Pept_S1A enterop.
InterPro; IPR001003; Pept_Ser_Cys.
InterPro; IPR001003; SEA.
InterPro; IPR001002; SEA.
InterPro; IPR001100; SICIT receptor.
Pfam; PF00431; CUB; 2.
Pfam; PF00629; NAM; 1.
Pfam; PF00629; NAM; 1.
Pfam; PF00629; NAM; 1.
Pfam; PF00639; SEA; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001138; Enteropeptidase; 1
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U09859; AAB40026.1; -
EMBL; L19663; AAA16035.1; -
PIR; A43090; A43090;
PDB; 1EKB; X-ray; A=788-800
MEROPS; S01.156; -
     DOMAIN
TOMAIN
DOMAIN
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PTM: The chains are derived from a single precursor cleaved by a trypsin-like protease.

SIMILARITY: Belongs to peptidase family S1.

SIMILARITY: Contains 2 CUB domains.

SIMILARITY: Contains 2 LDL-receptor class A domains.

SIMILARITY: Contains 1 MAM domain.

SIMILARITY: Contains 1 SEA domain.

SIMILARITY: Contains 1 SEA domain.
                                                                                                                                                                                                                                                                                                                       non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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; Peptidase_S1A.
pept_S1A_enterop.
; Pept_Ser_Cys.
; SEA.
; SEA.
chor; Transmembrane; Zymogen:
Chor; Transmembrane; Zymogen:
Enteropeptidase non-catalytic chain.
Enteropeptidase catalytic chain.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
SEA.
LDL-receptor class A 1.
CUB 1.
MAM.
CUB 2.
LDL-receptor class A 2.
SECR.
SECR.
Serine protease.
Charge relay system (By similarity).
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n; Myristate; Repeat;
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N-linked (GLONAC.
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                                             "Corin, a ...
from human heart
niol. Chem.
                                                                                                                                                                                                                                                                                               CORI HUMAN STANDARD; PRT; 1042 AA. 09Y5Q5; 09UHY2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Atrial natritteric peptide-converting enzyme (EC 3 converting enzyme) (Corin) (Heart specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 24
HUMAN
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STRAND
                                                                           Yan W., Sheng N., Seto M., More "Corin, a mosaic transmembrane from human heart.";
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                     Name=CORIN; Synonyms=CRN;
Homo sapiens (Human).
                                                                                                               MEDLINE=99262646; PubMed=10329693; Yan W., Sheng N., Seto M., Morser J.,
                     SEQUENCE OF
                                                                                                                                                           TISSUE=Heart;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=9606;
     TISSUE=Heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQGSTADVLQEADVPLLSNEK
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1007
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                     FROM
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                     N.A.
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Pred. No. 6.9e-41;
)1; Mismatches 187;
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     InterPro; IPR001217; LDL receptor A.
InterPro; IPR001217; LDL receptor A.
InterPro; IPR001214; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001903; Pept Ser_Gys.
InterPro; IPR00199; Srcr_receptor Pefam; Peptidase S1.
InterPro; IPR00199; Fri 2.
Pfam; Peptidase Fri 2.
Pfam; Peptidase Fri 2.
Pfam; Peptidase Fri 2.
Pfam; Peptidase Fri 2.
PRINTS; PR00725; Ld1 recept a; 6.
PRINTS; PR00725; CHYMOTRYPSIN.
PRINTS; PR00725; LDLRA 1; 6.
PROSITE; PS50038; F7; 2.
PROSITE; PS50038; F7; 2.
PROSITE; PS500420; SRCR_1; FALSE NEG.
PROSITE; PS500420; SRCR_1; FALSE NEG.
PROSITE; PS500420; TRYPSIN DM; 1.
PROSITE; PS500430; TRYPSIN DM; 1.
PROSITE; PS500134; TRYPSIN SER; 1.
PROSITE; PS500134; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005887; C:integral to plasma membrane; 7
GO; GO:0004252; F:serine-type endopeptidase acti
GO; GO:0006629; P:lipid metabolism: TAS.
GO; GO:0009653; P:morphogenesis; TAS.
GO; GO:00096508; P:proteolysis and peptidolysis;
GO; GO:0008217; P:regulation of blood pressure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
MIM; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF133845; AAD31850.1; -.
EMBL; AF113248; AAF21966.1; -.
HSSP; P01130; 1AJJ.
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-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 frizzled (FZ) domains.
-!- SIMILARITY: Contains 7 LDL-receptor class A domains.
-!- SIMILARITY: Contains 1 SRCR domain.
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Genew; HGNC:19012; CORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               natriuretic peptide-converting enzyme.";
Proc. Natl. Acad. Sci. U.S.A. 97:8525-8529(2000)
-!- FUNCTION: Converts Pro-AMP to AMP. Cleaves P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yan W., Wu F., Morser J., Wu Q.; "Corin, a transmembrane cardiac serine protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hooper J.D., Scarman A.L., Clarke B.E., No "Localization of the mosaic transmembrane
                                                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20359740; PubMed=10880574; DOI=10.1073/pnas.150149097;
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                                                                                                                                                                                             ransmembrane
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SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: Highly expressed in heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605236;
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                                                                                                                                                                                                               Hydrolase;
     1042
259
304
340
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LDL-receptor class I
LDL-receptor class I
LDL-receptor class I
LDL-receptor class I
FZ 2.
                                                                                             Signal-anchor for type II protein (Potential).
Extracellular (Potential)
FZ 1.
                                                                                                                                                                           Cytoplasmic
                                                                                                                                                                                                             Serine protease;
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ne serine protease
                                                                                                                                                                           (Potential)
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                       4 2 2 1
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Best Local Sim
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                                                                                                                                                                                                                                       RKELRCDGWADCTDHSDELNCSCDAGHQFTC-KNKFCKPLFWVCDSVNDCGDNSDEQGCS
                                                                                                                                                                                                                                                                                     WPEDTDCSQFPEENSDNQTCL-----MPDEYV-----EECSPSHFKCRSGQCV
                                                                                                                                                                                                                                                                                                                         YCGER---SQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPC-PGQFTCRTGRCI
                                                                                                                                                                                                                                                                                                                                                                    VQTNCYKYLMFFSCT--ILVP----KCDVNTGERIPPCRALCEHSKERCESVLGIVGLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRK-AQGTFNSPYYPGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCSVIQTSCQEGDQRCLYNPCLDSCG--GSSLCDPNNSLNNCSQCEPITL-ELCMNLP--
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ECDGKEDCSDGSDEKDCDCGLRSFTR-QARVVGGTDADEGEWPWQVSLHALGQGHICGAS 472
                                        CADGWQEILSQLACKQMGLGEPSVTKLIQEQEKEPRWLTLHSNWESLNGTTLHELLVNGQ
                                                                                                                      FCQDDELECANHACVSRDLWCDGEADCSDSSDEWDCVTLSINVNSSSFLMVHRAATEHHV
                                                                                                                                                          - CPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNV---------
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Serine protease.

Charge relay system (By similal Charge relay system.)

Charge relay system.

Serine protease.

Serine Serine Serine (Serine)

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Serine (Serine)
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Pred. No. 3.3e-40;
5; Mismatches 259; Indels 180;
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RESULT
Q80YN4
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Langenickel T., Pagel I., Buttgereit J., Tenner K., Lindner Willenbrock R., Dietz R., Bader M.;
Willenbrock R., Dietz R., Bader M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; AY251285; AAO86772.1; -.
EMBL; AY251285; AAO86772.1; -.
EMBL; AY251285; AAO86772.1; -.
EMSEP; OO7954; ICR8.
GO; GO:001620; C:membrane; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:000544; F:scavenger receptor activity; IEA.
GO; GO:000544; F:scavenger receptor activity; IEA.
GO; GO:00057275; P:development; IEA.
GO; GO:0007275; P:development; IEA.
GO; GO:0007275; P:development; IEA.
Query Match
Best Local Similarity
                                                                                                    SMART; SM00192; LDLa; 7.

SMART; SM00202; SR; 1.

SMART; SM00020; Tryp_SPc; 1.

SMOSITE; PS50038; FZ; 2.

PROSITE; PS50038; FZ; 2.

PROSITE; PS50068; LDLRA_1; 6.

PROSITE; PS50079; SRCR_2; 1.

PROSITE; PS50079; SRCR_2; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50135; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                PRINTS;
PRINTS;
SMART; S
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01-JUN-2003
01-MAR-2004
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Q80YN4;
                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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InterPro; IPR002172; LDL receptor A.
InterPro; IPR0012172; LDL receptor A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
InterPro; IPR001190; Srcr_receptor.
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PF00087; Ldl recept a; 6.
PF00089; Trypsin; 1.
                                                                                                                                                                                                                                                                                                       ; PR00722; CHYMOTRYPSIN; PR00261; LDLRECEPTOR. SM00063; FRI; 2.
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                                                               Protease;
1111 AA;
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Last annotation updat
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Score 690.5; DB 2; Pred. No. 6.2e-40;
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                 3BA2706CBE81157F CRC64;
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                    Length 1111;
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                                                                                                                                                                                                                                                                                                                                 Q8CAN9;
                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched
STRAIN=C57BL/6J;
                      SEQUENCE FROM N.A
                                                                                                                                                                                       full insert sequence.
                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                             ibrary, clone:A130097D21 product:protease, serine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISWESALFPALVQTNCYKYLMFFACTILVPKCDVNTGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKVLGPGVYSNVSYFVDWIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEQCQSYFDMKTITNRMICAGYESGTVDSCMGDSGGPLVCERPGGQWTLFGLTSWGSVCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEK----DCDCGLRSFTR-QARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QETLSQLACROMGLGEPSVTELVQGQEGQQWLRLHSSWENLNGSTLQELLVHRRSCPSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHECVPRDLWCDGWTDCSDSSDEWGC----VTLSKNGNSSSFLTVHRSARDHHVCADGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~-SCVESCAGSSLCDSDSSLSNCSHCEPITL-ELCMNLP--YNLTHYPNYLGHRTQKEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QR-NKPGVYTRLPLFRDWIK 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SSONVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHYPP-NI
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                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
TISSUE=Thymus;
                                                                                                                                                                                         (Fragment).
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                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                            PRT;
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  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

-! SIMILARITY: Belongs to peptidase family S1.

C -!- SIMILARITY: Contains 1 MAM domain.

R EMBL; AK038356; BAC29973.1; --

R MGD; MGI:1117523; Prss7.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016201; F:chymotrypsin activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:000823; F:schymotrypsin activity; IEA.

R GO; GO:000823; F:schymotrypsin activity; IEA.

R GO; GO:000829; F:trypsin activity; IEA.

R GO; GO:0005044; F:scavenger receptor activity; IEA.

R GO; GO:0006295; F:trypsin activity; IEA.

R GO; GO:0006598; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000859; CUB.

R InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FOR THE STRAIN-CSPEL/6J; TISSUE=Thymus; STRAIN-CSPEL/6J; TISSUE=Thymus; STRAIN-CSPEL/6J; TISSUE=Thymus; STRAIN-CSPEL/6J; TISSUE=Thymus; Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Haraoka T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka I., Kasukawa T., Konio H., Kouda M., Koya Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Thymus;

MEDILINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Cannama Ros 10.1757-1771(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibatkonno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                      InterPro;
InterPro;
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STRAIN=C57BL/6J; TISSUE=Thymus;
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[4]
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
[3]
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ficiency full-length cDNA cloning.";
zymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                        IPR000998;
IPR001254;
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                                                 MAM.
Peptidase_S1A
                      Peptidase_S1
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PROSITE; PS01180; CUB; 1.

PROSITE; PS01209; LDLRA_1; 1.

PROSITE; PS00606; LDLRA_2; 1.

R PROSITE; PS00740; MAM_1; UKNONN_1.

R PROSITE; PS50060; MAM_2; 1.

R PROSITE; PS50287; SRCR_2; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN SER; 1.

Glycoprotein; Hydrolase; Kinase; Protease; S
NON TER

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Best Local :
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Pfam; PF00629; MAM; 1.

Pfam; PF00629; MAM; 1.

Pfam; PF00629; SRCR; 1.

Pfam; PF00530; SRCR; 1.

Pfam; PF00530; SRCR; 1.

PFINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00722; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00192; LDLa; 1.

SMART; SM00192; LDLa; 1.

SMART; SM00137; MAM; 1.

SMART; SM00137; MAM; 1.

SMART; SM00020; Tryp_SPC; 1.
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                643
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                                                                                                                                                                               H---ICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVFNAFRNRGCSTIALDDISLTNGICSQSPYPEPTLVPTPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLI 145
DGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWI
                                                                                                                                RIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQY
                                                                                                                                                                                                                       LQCSQDSLILLQCNHKS-----CGEKKVTQKVSPKIVGGSDAQAGAWPWVVALYHRDRS
                                                                                                                                                                                                                                                                                                            GKCLSKSQQCNGKDDCGDGSDEASCP-----KVNVVTCTKHTYRCLNGLCLSKGN 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHVKVRFKFFYLLEPRRACGTCPKDYVEI--NGE-----KYCGERSQFVVTSNSNKIT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNTERRHPGFEATFFQLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNN
                                          GGTGALILQKGEIRVINQTTCENLLPQ-QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEA
                                                                                                                                                                                                                                              PECDGKE----DCSDGSDEKDCDCGLRSFTROA--RVVGGTDADEGEWPWQVSLHALGQG
                                                                                                                                                                                                                                                                                 EVC----
                                                                                                                                                                                                                                                                                                                                         EASCVRFLNGTRSNNGLVQFNIHS----IWHI----ACAEN--
                                                                                                                                                                                                                                                                                                                                                                        ELNC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNIQLHFQEFDLEN-----INDVVEVRDGGEFDSLLLAVYTGPGPVKDLFSTTNRMT
                                                                                                    QIVINPHYDRRRKVNDIAMMHLEFKVNYTDYIQPICLPEENQIFIPGRTCSIAGWGYDKI
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29.3%;
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Pred. No. 6.2e-40;
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A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
A Soeda E., Ohki M., Takagi T., Sakaki Y., Tudien S., Blechschmidt K.,
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A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
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A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand B.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand B.,
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"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                   Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.;
"Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of a distinctive assortment of domains.";
Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
-!- FUNCTION: Responsible for initiating activation of pancreatic proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptida A). It catalyzes the conversion of trypsinogen to trypsin which turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases.
-!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-[-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND DISEASE.
SEQUENCE FROM N.A., AND DISEASE.
MEDLINE=21606074; PubMed=11719902;
Holzinger A., Mater E.M., Buck C., Mayerhofer P.U., Kappler M. Holzinger A., Mater E.M., Buck C., Sadler J.E., Roscher Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher "Mutations in the proenteropeptidase gene are the molecular congenital enteropeptidase deficiency.";
Am. J. Hum. Genet. 70:20-25(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95234679; PubMed=7718557; Kitamoto Y., Veile R.A., Donis-Keller H., Sa "CDNA sequence and chromosomal localization proteolytic activator of trypsinogen."; Biochemistry 34:4562-4568(1995).
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01-FEB-1996 (Rel. 33, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P98073;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94329561; PubMed=8052624;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 749-1019 TISSUE=Duodenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20289799; PubMed=10830953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PRSS7; Synonyms=ENTK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
trypsinogen.
SUBUNIT: Heterodimer of a catalytic (light) chain and a multidomain (heavy) chain linked by a disulfide bond.
multidomain (heavy) chain linked by a disulfide bond.
SUBCELLULAR LOCATION: Type II membrane protein (Probable).
TISSUE SPECIFICITY: Intestinal brush border:
PYM: The chains are derived from a single precursor that is cleaved by a trypsin-like protease.
DISEASE: Defects in PRSS7 are a cause of enterokinase deficiency [MIM:228200]; a life-threatening intestinal malabsorption disord characterized by diarrhea and failure to thrive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :••
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
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on of human
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MIN; 22230;

MIN; 22230;

GO: GO:005903; C:brush border; TAS.

InterPro; IPR002172; LDL receptor A.

InterPro; IPR001274; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR0013163; Peptidase_S1.

InterPro; IPR001163; Pept_Sar_cys.

InterPro; IPR001082; SEA.

InterPro; IPR000082; SEA.

InterPro; IPR000190; Srcr_receptor.

Pfam; PF00431; CUB; 2.

Pfam; PF00431; CUB; 2.

Pfam; PF00629; MAM; 1.

Pfam; PF00530; SECR; 1.

Pfam; PF00530; SECR; 1.

Pfam; PF00530; SECR; 1.

Pfam; PF00530; SECR; 1.

PFAMP; PR00722; CHYMOTRYPSIN.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00721; LDLRECEPTOR.

PRINTS; PR000261; LDLRA_1; 2.

PROSITE; PS01209; LDLRA_1; 2.

PROSITE; PS01209; LDLRA_2; 2.

PROSITE; PS01209; LDLRA_2; 1.

PROSITE; PS01209; LDLRA_2; 1.

PROSITE; PS01209; LDLRA_2; 1.

PROSITE; PS01209; LDLRA_2; 1.

PROSITE; PS05068; MAM_2; 1.

PROSITE; PS05068; MAM_2; 1.

PROSITE; PS05024; SEAF; 1.

PROSITE; PS05024; SECR_1; PALSE_NEG.

PROSITE; PS05027; SRCR_1; PALSE_NEG.

PROSITE; PS050287; SRCR_1; PALSE_NEG.

PROSITE; PS050287; SRCR_1; PALSE_NEG.
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                                                                                                 m; PF00431; CUB; 2.
m; PF00057; Ldl recept_a; 2.
m; PF000629; MAM; 1.
im; PF00530; SEA; 1.
im; PF00530; SRCR; 1.
im; PF00089; Trypsin; 1.
im; PF00089; Trypsin; 1.
im; PF000722; CHYMOTRYPSIN.
INTS; PR00722; CHYMOTRYPSIN.
INTS; PR00261; LDLAECEPTOR.
INTS; PR002620; MAMDOMAIN.
                                                                                                                                                                                                                                                                                                                                       new; HGNC:9490; PRSS7.
V; 606635; -.
V; 226200; -.
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Y19131; CAB65555

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: Contains 2
: Contains 2
: Contains 1
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2 CUB domains.
2 LDL-receptor class A |
1 MAM domain.
1 SEA domain.
1 SRCR domain.
                                                                                                                                             1.
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                270
                                 576
                                                                                161 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP
                                                                                                  180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease;
                                                                                                          Similarity
                                                                 ELP-
               AEYLS---YDSSDPCPG-QFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQF---
ANFTTGYHLGIPEPCKADHFQCKNGECVPLVNLCDGHLHCEDGSDEADCV-----RFFNG
                                                 RRACGTCPKDYVEI-NGEK-----
                                                                                                                                   1019
                                                                                                                                                   Conservative
                                                                 -TDCGGPFELWEPNTTFSSTNFPNSYPNLAFCVWILNAQKGKNIQLHFQEFDLEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
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                                 - INDVVEIRDGEEADSLILLAVYTGPGPVKDVFSTTNRMTVLLITNDVLARGGFK
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169
223
334
504
634
679
771
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Q -> E (in Ref. 3).
S -> P (in Ref. 3).
SQCCLQDSLIRLQCNHKS -
Ref. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hor; Transmembrane; Zymogen.
Enteropeptidase non-catalytic chain.
Enteropeptidase catalytic chain.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                      Interchain (By By similarity. By similarity. By similarity. By similarity. By similarity. N-linked (Glow).
                                                                                                                                                                                                                                                                                                                                                                      By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                        Charge relay system Charge relay system Charge relay system N-myristoyl glycine
                                                                                                 Score 683.5; DB 1
Pred. No. 1.7e-39;
0; Mismatches 202
                                                                                                                                                                                    N-linked
N-linked
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N-linked
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N-linked
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N-linked
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                                                 YCGERSQFVVTSNSNKITVRFHSDQSYTDTGFL
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H (GleNAC...
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H (GLENAC.
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(By similarity).
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(Potential).
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(Potential)
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(Potential).
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(Potential).
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ENTK MOUSE
P97435;
01-NOV-1997
 This SWI
between
the Euro
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Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., Sadder J.E.;
"Structure of murine enterokinase (enteropeptidase) and expression in small intestine during development.";
Am. J. Physiol. 274:G342-G349(1998).
-I- FUNCTION: Responsible for initiating activation of pancreatic proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase A). It catalyzes the conversion of trypsinogen to trypsin which in turn activates other proenzymes including chymotrypsinogen, procarboxypeptidases, and proelastases (By similarity).
-I- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Enteropeptidase (EC 3.4.21.9) (Enterokinase).
Name=Prss7; Synonyms=Entk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Duodenum;
                                               similarity).

SUBCELLULAR LOCATION: Type II membrane protein (Probable)
PYM: The chains are derived from a single precursor that
cleaved by a trypsin-like protease (By similarity).
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 2 LDL-receptor class A domains.
SIMILARITY: Contains 1 MAM domain.
SIMILARITY: Contains 1 SRA domain.
SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                      trypsinogen.
SUBUNIT: Heterodimer of a
                                                                                                                                                                            multidomain (heavy)
                          SWISS-PROT
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             the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCKN----KFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDC
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Swiss Institute
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                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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  PROSITE; PS01180; ĈŪĒ; 2:
PROSITE; PS01209; LDLRA 1; 2:
PROSITE; PS50068; LDLRA 2; 2:
PROSITE; PS50060; MAM 1; 1.
PROSITE; PS50060; MAM 2; 1.
PROSITE; PS50044; SEA; 1.
PROSITE; PS500420; SRCR 1; PALSE; PROSITE; PS50240; SRCR 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1
PROSITE; PS502140; TRYPSIN HIS; 1.
PROSITE; PS50134; TRYPSIN HIS; 1.
PROSITE; PS50134; TRYPSIN BER; 1.
PROSITE; PS50135; TRYPSIN BER; 1.
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SMART; SM00137;
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Pfam;
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PIRSF; PIRSF001138; Enteropeptidase;
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HSSP; P98072; 1EKB.
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InterPro; IPR001314;
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PF00057; Ldl_recept_a;
PF00629; MAM; 1.
PF01390; SEA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                       FALSE_NEG.
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By similarity.
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                          similarity).
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Pred. No. 4.9e-39;
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        InterPro; IPRO0173; Fz domain.

InterPro; IPRO0173; LDL receptor A.

InterPro; IPRO01314; Peptidase S1.

InterPro; IPRO01314; Peptidase S1.

InterPro; IPRO01393; Pept Ser Öys.

InterPro; IPRO01993; Pept Ser Öys.

InterPro; IPRO01993; Pept Ser Öys.

InterPro; IPRO0199; Srcr_receptor.

Pfam; PP00057; Ldl_recept_a; 6.

Pfam; PP00057; Ldl_recept_a; 6.

Pfam; PR00122; CHYMOTRYPSIN.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR000261; LDLRECEPTOR.

SMART; SM000065; FRI; 2.

SMART; SM000065; FR; 1.

SMART; SM000020; SR; 1.

SMART; SM000020; SR; 1.

SMART; SM000020; TryP_SPC; 1.

SMART; SM000020; TryP_SPC; 1.

PROSITE; PS001209; LDLRA_1; 6.

PROSITE; PS001209; LDLRA_2; 7.

PROSITE; PS001209; LDLRA_2; 7.

PROSITE; PS001209; SRCR_1; FALSE_NEG.

PROSITE; PS00287; SRCR_2; 1.

PROSITE; PS00287; SRCR_2; 1.

PROSITE; PS001315; TRYPSIN JOM; 1.

PROSITE; PS001315; TRYPSIN SER; 1.

PROSITE; PS001315; TRYPSIN SER; 1.

PROSITE; PS001315; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- FUNCTION: Converts pro-ANP to ANP. Cleaves pro-
between Arg-122 and Ser-123 (By similarity).
-:- SUBCELLULAR LOCATION: Type II membrane protein.
-:- TISSUE SPECIFICITY: Highly expressed in heart.
-:- SIMILARITY: Belongs to peptidase family S1.
-:- SIMILARITY: Contains 2 frizzled (FZ) domains.
-:- SIMILARITY: Contains 7 LDL-receptor class A dom
-:- SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDILINE=98429596; PubMed=9756624;

MEDILINE=98429596; PubMed=9756624;

Tomita Y., Kim D.-H., Magoori K., Fujino T., Yamamoto T.T.;

Tomita Y., Kim D.-H., Magoori K., Fujino T., Yamamoto T.T.;

Tomita Y., Kim D.-H., Magoori K., Fujino T., Yamamoto T.T.;

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16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Atrial natriuteric peptide-converting enzyme (EC 3.4.21.-) (pro-ANP-converting enzyme) (Corin) (Low density lipoprotein receptor related
                                                                                                                                                                                Transmembrane.
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HSSP; P01130; 1AJJ.
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Mammalia; Eutheria;
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Cytoplasmic (Potenti
Signal-anchor for ty
protein (Potential).
Extracellular (Poten
FZ 1.
LDL-receptor class A
LDL-receptor class A
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                                                                                                                                                                                                                                   Serine protease;
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                                                                                               MCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQR-NKPGVYTRLPLFRD
                                                                                                                                                                                         DVWKVVFGINNLDHPSG-FMQTRFVKTILLHPRYSRAVVDYDISVVELSDDINETSYVRP
                                                                                                                                                                                                             TQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRP
                                                                                                                                                                                                                                                 RMNKRILGGRTSRPGRWPWOCSLOSEPSGHICGCVLIAKKWVLTVAHCF-EGR----EDA
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                                                                                                                                 VCLPSPEEYLEPDTYCYITGWGH--MGNKMPFKLQEGEVRIIPLEQCQSYFDMKTITNRM
                                                                                                                                                  -LSKGNPECDGKE-----DCSDGSDEKD------C---DCGLRSFT
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:ceptidase activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001272; LDL_receptor A.

R InterPro; IPR001314; Peptidase_S1A.

R InterPro; IPR001314; Peptidase_S1A.

R InterPro; IPR001314; Peptidase_S1A.

R InterPro; IPR0013190; Srcr_receptor.
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PRINTS; PRO0721; LDLREEEPTOR.
SMART; SM00102; LDLR; 8.
SMART; SM00102; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM001020; LDLRA, 1; 8.
PROSITE; PS00104; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; PS01105; TRYPSIN_SER; 1.
Hydrolase; PS01105; TRYPSIN_SER; 1.
Hydrolase; PS01105; TRYPSIN_SER; 1.
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Q9DGR2;
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01-MAR-2001
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-|- SIMILARITY: Belongs to |
EMBL; AB038497; BAB08217.1;
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Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
Embryonic Berine protease-2.
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MEDLINE=20363741; PubMed=10903452;
Yamada K., Takabatake T., Takeshina K.;
"Isolation and characterization of three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00057; Ldl_recept_a; 4. Pfam; PF00089; Trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Xenopus Laevis."
Gene 252:209-216(2000)
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DCGDGSDEASC-PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDC-----
                                             AYOMCDGVROCYYGDDERNCVTATTTTATTTSPPTCQIYCMNFMYYYTCIYAYOMCDGVR
                                                                                                                                                                NCATKTPSIPTCOMYC--SYTSTCIYGYQI---
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                                                                         LFWVCDSVNDCGDNSDEQGC---
                                                                                                      PTCQLYCSYYYTCIYAYQICNGVLDCPFVDDERNCVIATTSTPTCQIYCWDFMFDYTCIY
                                                                                                                                 ------RCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCK-----
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Pred. No. 7e-37;
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membrane-bound arginine-specific serine proteinase precursor - r (;Species: Rattus norvegicus (Norway rat) C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: JC7731; JC7775 R;Kishi, K.; Yamazakk, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; J. Biochem. 130, 425-430, 2001 A;Title: Characterization of a membrane-bound arginine-specific A;Reference number: JC7731; MUID:21421307; PMID:11530019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-855 <SATS
A;Cross-references: DDBJ:AB037898
C;Comment: This enzyme, an epithelial-derived, type II integral of specific proteins or peptides on the brushborder membranes.
Lial migration and/or cell loss.
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A;Experimental source: strain Male, 7-week-Oni, Y.; Iwanaga, T.; Fushiki, R;Satomi, S.; Yamasaski, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, Biochem. Biophys. Res. Commun. 287, 995-1002, 2001
A;Title: A role for membrane-type serine protease (MT-SP1) in intestinal epa;Reference number; JC7775; PMID:11573963
A;Contents: Small intestine
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                                                                                                       SNGKCLPQSQQCNGKDDCGDGSDEASCDNVNAVSCTKYTYRCQNGLCLNKGNPECDGKKD
                                                                                                                                                                                                            GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                    CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                          SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                             GWADCPDYSDERHCRCNATHQFMCKNQFCKPLFWVCDSVNDCGDGSDEEGCSCPAGSFKC
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83.0%; Pred. No. 3.70
tive 59; Mismatches
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F;541-646/Domain: Clr/Cls repeat homology <ClR>
F;658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;693-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <S
F;800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F;800-1029/Domain: trypsin homology <TRY>
F;116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902,
F;807-911,825-841,925-992,956-971,982-1010/Disulfide bonds: #status predicted
F;840,891,986/Active site: His, Asp. Ser #status predicted
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A;Moccession: A53663
A;Molecule type: mRNA
A;Residues: 1-1034 <MAT>
A;Residues: 1-1034 <MAT>
A;Cross-references: GB:D30799; NID:g505122; PIDN:BAA06459.1; PID:g505123
A;Cross-references: GB:D30799; NID:g505122; PIDN:BAA06459.1; PID:g505122; PID:g505122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 ELP--TDCGGPFELWEPNTTFTSMNFPNNYPNQAFCVWNLNAQKGKNIQLHFEEFDLEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP
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C;Function:
A;Bescription: cleaves propeptide from trypsinogen to produce active trypsin A;Bescription: cleaves propeptide from trypsinogen to produce active trypsin A;Besthway: intestinal digestive hydrolase cascade
C;Superfamily: enteropeptidase; Clr/Cls repeat homology; LDL receptor ligand
C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmemb
F;22-38/Domain: transmembrane #status predicted <TMM>
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1035 <KIT>
A;Cross-references: UNIPROT:P98072; GB:U09859; NID:974641
A;Experimental source: small intestine
R;LaVallie, B.R.; Rehemtulla, A.; Racie, L.A.; DiBlasio,
J. Biol. Chem. 268, 23311-23317, 1993
A;Title: Cloning and functional expression of a cDNA enco
A;Reference number: A48874; MUID:94043122; PMID:8226855
A;Accession: A48874
                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 801-807,'Y', 809-827 <LIG>
C;Comment: The mechanism of association with the membrane of the embrane attachment using a signal-anchor sequence.
C;Comment: Conversion from membrane-bound to soluble forms may in C;Complex: mature enteropeptidase is variously reported to contailfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E. Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, A;Reference number: A43090; MUID:94329561; PMID:8052624
A;Accession: A43090
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A43090
enteropeptidase (EC 3.4.21.9) pi
enteropeptidase (EC 3.4.21.9) pi
N;Alternate_names; enterokinase
                                                                                                                                                                                                                                                                                                                                                                             A; Title: The amino-terminal sequence of the catalytic subunit A; Reference number: A61436; MUID:92189715; PMID:1799406 A; Accession: A61436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 801-1035 <LAV>
A;Residues: 801-1035 <LAV>
A;Cross-references: GB:L19663; NID:g416131; PIDN:AAA16035.1; PID:g416132
A;Note: parts of the mature pro
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J. Protein Chem. 10, 475-480, 1991
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F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;358-520/Domain: MAM homology <MAM>
F;358-520/Domain: CLT/C1s repeat homology <CLR>
F;654-647/Domain: CLT/C1s repeat homology <CLR>
F;659-693/Domain: LDL receptor ligand-binding repeat homology *status atypical <SRC!
F;694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC!
F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>
F;801-1030/Domain: trypsin homology <TRY>
F;116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Binding
F;788-912,826-842,926-993,957-972,983-1011/Disulfide bonds: #status predicted
F;841,892,987/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LGTGNSSVPTFSTGGGPYVNLNTAP-----NGSLILTPSQQC-----LEDSLILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRACGTCPKDYVEI-NGEKYCGERSQFV-----VTSNSNKITVRFHSDQSYTDT
                                           KPGVYTRLPLFRDWIK 678
                                                                                                                                                                             HLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQGSTADVLQEADVPLLSNEK
                                                                                                                                                                                                                    ELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTT 603
                                                                                                                                                                                                                                                                                                       HCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALL 543
                                                                                                                                                                                                                                                                                                                                                          QCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAA
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                                                                                     CQQQMPEYNITENMVCAGYEAGGVDSCQGDSGGPLMCQE-NNRWLLAGVTSFGYQCALPN
                                                                                                                               CENTLPQ-QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRN
                                                                                                                                                                                                                                                                  HCVYG----RNMEPSKWKAVLGLHMASNLTSPQIETRLIDQIVINPHYNKRRKNNDIAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFKANFTTGYGLGIPEPCKEDNFQCKDGECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTT 701
RPGVYARVPRFTEWIQ
                                                                                                                                                                                                                                                                                                                                                                                               DCD----CGLRSFTRQA--RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDDCGDGSDEASC-----PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSSGLVQFRIQS-----IWHV----ACAEN-------WTTQISDDVC-----QLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAGH--QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNG 374
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RESULT 4
A56318
A56318
enteropeptidase (EC 3.4.21.9) precursor [validated] - human
N;Alternate names: enterokinase
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: A56318; B43090
R;Kitamoto, Y; Veile, RA.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A;Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic A;Reference number: A56318; MUID:95234679; PMID:7718557
A;Accession: A56318
A;Residues: 1-1019 <KIT>
A;Rcross-references: UNIPROT:P98073; GB:U09860; NID:g746412; PIDN:AAC50138.1; PID:g746413
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994

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Gucts.

C;Function:
C;Function
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A;Cross references: GDB:384083; OMIM:226200
A;Map position: 21q21-21q21
C;Complex: Mature enteropeptidase is variou ed by a disulfide bond. Possibly, conversion
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A;Accession: B43090
A;Atsatus: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 749-1019 <KI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                            LLPQ-QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPG
                                                                                                 FKVNYTDY1QP1CLPEENQVFPPGRNCS1AGWGTVVYQGTTAN1LQEADVPLLSNERCQQ
                                                                                                                                                     KPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCEN
                                                                                                                                                                                                                                                            IDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELE
                                                                                                                                                                                                                                                                                                                                                EKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDG-----KEDCSDGS-----D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEYLS --- YDSSDPCPG-QFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRACGTCPKDYVEI-NGEK-----YCGERSQFVVTSNSNKITVRFHSDQSYTDTGFL
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                                                                                                                                                                                                                                                                                                                    HKSCGKKLAAQDITPKIVGGSNAKEGAWPWVVGLY-YGGRLLCGASLVSSDWLVSAAHCV
                                                                                                                                                                                                                                                                                                                                                                                                                             GLGSGNSSKPIFST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCKN----KFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDC
                                                                                                                                                                                                       YG----RNLEPSKWTAILGLHMKSNLTSPQTVPRLIDEIVINPHYNRRKDNDIAMMHLE
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                                                                                                                                                                                                                                                                                                                                                                                                                        ----DGGPFVKLNTAPDGHLILTPSQQCLQDSLIRLQCN
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32.7%;
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C;Superfamily: mouse low-density lipoprotein receptor-related protein; F;337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1> F;3374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2> F;410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3> F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4> F;648-82/Domain: LDL receptor ligand-binding repeat homology <LDL5> F;648-720/Domain: LDL receptor ligand-binding repeat homology <LDL6> F;648-720/Domain: LDL receptor ligand-binding repeat homology <LDL6> F;723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>
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R;Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.

J. Biochem. 124, 784-789, 1998

A;Title: A novel low-density lipoprotein receptor-related protein with A;Reference number: JE0315; MUID:98429596; PMID:9756624

A;Accession: JE0315
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C;Species: Mus musculus (house mouse)
C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 09-Jul-2004
C;Accession: JE0315
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A;Residues: 1-1113 <TOM>
A;Cross-references: UNIPROT:Q9Z319; DDBJ:AB013874; NID:g3869144; PIDN:BAA34371.1; PID:g38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 RFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GWVDCSDSSDEWGCVTLSKNGNSSSLLTVHKSAKEHHVCADGWRETLSQLACKQMGLGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKERALWECPFNKQCLKHTLICDGFPDCPDSMDEKNCSFCQDNELECANHECVPRDLWCD
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I CAGYESGTVDSCMGDSGGPLVCERPGGQWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVG
                                                                   MCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQR-NKPGVYTRLPLFRD
                                                                                                                                                                                                         ICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQ-ITPRM
                                                                                                                                                                                                                                                                                       DVWKVVFGINNLDHPSG-FMQTRFVKTILLHPRYSRAVVDYDISVVELSDDINETSYVRP
                                                                                                                                                                                                                                                                                                                                                          TOWTAFLGLHDOSORSAPGVOERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                 RMNKRILGGRTSRPGRWPWQCSLQSEPSGHICGCVLIAKKWVLTVAHCF-EGR----EDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTKLIPGQEGQQWLRLYPNWENLNGSTLQELLVYRHSCPSRSEISLLCSKQDCGRRPAA
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                                                                                                                                             VCLPSPEEYLEPDTYCYITGWGH--MGNKMPFKLQEGEVRIIPLEQCQSYFDMKTITNRM
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Pred. No. 4.7e-36;
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polyprotein - African clawed frog (Species: Xenopus laevis (African clawed frog) (Species: Xenopus laevis (African clawed frog) (C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004 C;Accession: T30337 R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L. submitted to the EMBL Data Library, March 1998 submitted to the EMBL Data Library, March 1998 A;Reference number: Z20829 A;Reference number: Z20829 A;Accession: T30337
Ra-reactive factor (EC 3.4.21.-) 1 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 1 (
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: I54763; JN0883
R;Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
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A; Residues: 1-1524 < YAN>
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                                                                                                                                                                        QFSIYGLVSWGEGCGRVSKPGVYTKVRLFFTWI-QNT
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                                                                                                                                                                                                        RIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENT
                                                                                                                                                                                                                                                                         GALILOKGEIRVINOTTCE-NLLPQQITPRMMCVGFLSG-GVDSCQGDSGGPLSSVEADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCSCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLS
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                                                                                                                                                                                                                                         PALGLQQLQLPILDSIICNTSYYSGELTDHMLCAGFPSSKEKDACQGDSGGPLVCQNEKE
                                                                                                                                                                                                                                                                                                             IHDNYNSETYDNDIALLYLEEPLDLNDFVRPVCLPEPEEVLTPASVCVVIGWGNTAEDGQ
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                                                                                                                                                                                                                                                                                                                                           SHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGT 586
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25.9%; Pred. No. 3.
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                                                                   precursor - human
protein-associated serine proteinase 1 (MASP-1)
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   NNLTTYKSEI---KYSCQE-----
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Int. Immunol. 6, 665-669, 1994
A;Title: Molecular characterization of a novel serine protease involved in activat A;Reference number: I54763; MUID:94289349; PMID:8018603
A;Reference number: I54763; MUID:94289349; PMID:8018603
A;Reference number: I54763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cession: I54763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-699 <AST>
A;Cross-references: UNIPROT:P48740; GB:D28593; NID:g790963; PIDN:BAA05928.1; PID:g
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins found in a bacteric. A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Residues: 1-234, E',236-284, G',286-498, K',500-542, K',544-642, S',644-699 <TAK
A;Cross-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
C;Comment: This is a serum bactericidal factor that activates complement C4 and C2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;185-294/Domain: Clr/Cls repeat homology <CIR2>
F;301-362/Domain: Clr/Cls repeat homology <FH1>
F;301-362/Domain: complement factor H repeat homology <FH2>
F;367-432/Domain: complement factor H repeat homology <FH2>
F;367-432/Domain: complement factor H repeat homology <FH2>
F;449-691/Domain: trypsin homology <TRY>
F;449-178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;49,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;49,1743-157,153-166,168-181,185-122,242-260,301-349,329-362,367-414,397-432,436-572,4
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
F;490,552,646/Active site: His, Asp, Ser #status predicted
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G;Superfamily: complement-activating serine proteases Clr/Cls/MASP; Clr/Cls repeat C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-448,449-699/product: Ra-reactive factor #status predicted <MAT>
F;19-135/Domain: Clr/Cls repeat homology <CIR1>
F;143-181/Domain: EgF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP
A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
                                                                       NGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRC-----LNGLCLSKGNPEC
                                                                                                                                                          KVLKDNVEMDTFQIECLKDGTWSNKIPTCKIVD
                                                                                                                                                                                                                                                                                                                     WRLSYRA--AGNECPELQPPVHGKIEPSQAKYFFK-----
                                                                                                                                                                                                                                                                                                                                                                                                FLAEYLSYDSSDPCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYLLEPRRACGTCPKDYVEIN-GEK----YCGERSQFVVTSNSNKITVRFHSDQSYTDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYILHTDNRTCRVECSDNLFTQRTGVITSPDFPNPYPKSSECLYTIELEEGFMVNLQFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSQNVLLITLITHTERRHPGFEATFFQLP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKASAHTVELNNMFG-----QIQSPGYPDS-YPSDSEVTWNITVPDGFRIKLYFMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKTVQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS
                                                                                                                                                                                                                                 QF----TCKNKFCKPLFW-----VCDSVNDCGDNSDEQGCSCPAQ-----TFRCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFDIQDHPEV-PCPYDYIKIKVGPKVLGPFCGEKAPEPISTQSHSVLILFHSDNSAENRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKF
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24.9%; Pred. No. 9.1e-30;
tive 112; Mismatches 272;
                                                                                                                                                                                                                                                                                                                                                                                            GOFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGH
- PYYKMLNNNTGIYTCSAQGVWMNKV-LGRSLPTC
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                                                                                                                                                          CRAPGELEHGLITFSTR 383
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C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F;1-19/Domain: signal sequence #status predicted <SIG*
F;20-390/Product: plasma kallikrein heavy chain #status experimental <HCH>
F;20-109/Domain: apple repeat <AP1>
F;20-109/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP2>
F;201-380/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-631/Domain: trypsin homology <TRY>
F;311-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasma kallikrein (EC 3.4.21.34) precursor - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date 30.5ep-192 #sequence_revision 30.5ep-192 #text C;Accession: A36557 R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaul R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaul DNA Cell Biol. 9, 737-748, 1990 A;Title: Mouse plasma kallikrein: cDNA structure, enzyme A;Reference number: A36557; MUID:91090844; PMID:2264928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P26262; GB:M58588; NID:9200358; PIDN:AAA63393.1; PID:9200355 A;Note: part of this sequence, including the amino ends of both the heavy and light charce; C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex v C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a 1:
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A; Residues: 1-638 < SEI>
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                                               CPKD-----YVEINGEKYCGERS---QFVVTSNSNKITVRFHSDQSYTDTG----FLAE
                                                                                               TWNFHCOF-FTYATSAFYRPEYRKKCLLKHSASGTPTSIKSADNLVSGFSLKSCALSEIG
                                                                                                                                                                                           SITGTLPRIHRTGAISGHSLKQCGHQISACHRDIYKGLDMRGSNFNISKTDNIEECQKLC
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                                                                                                                                                                                                                                                                                          RGGDLAAIYTP----DAQYCQKMCTFHPRCLLFSF-----
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  CPMDIFQHSAFADLNVSQVITPDAFVCRTICTFHPNCLFFTFYTNEWETESQRNVCFLKT
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27.5%;
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                                                                                                                                                                                                                                                                                                                                                                               Score 545.5; DB 1;
Pred. No. 1.6e-28;
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KQRTPL

Fightsma kallikrein (EC 3.4.21.34) precursor - rat

plasma kallikrein (EC 3.4.21.34) precursor - rat

N;Alternate names: Fletcher factor; kininogenin; serum kallikrein

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: A39180; A33320; So6851; I53044; S06852

R;Beaubien, G; Rosinski-Chupin, I; Mattei, M.G.; Mbikay, M.; Chretien, M.;

Biochemistry 30, 1628-1635, 1991
                                                                 A; Molecule type: protein
A; Residues: 20-45;391-413 <PAQ>
R; Seidah, N.G.; Ladenheim, R.; P
DNA Cell Biol. 8, 563-574, 1989
A; Title: The CDNA structure of 1
                                                                                                                                                                                                               A;Cross-references: GB:M30282; NID:g205010; PIDN:AAA41463.1; PID:g205011 A;Note: part of this sequence, including the amino ends of both the heavy R;Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, Biochim. Biophys. Acta 999, 103-110, 1989

A;Title: Rat plasma Kallikrein: purification, NH(2)-terminal sequencing an A;Reference number: S06851; MUID:90089457; PMID:2597701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P14272; GB:J05315
A;Note: the authors translated the codon GAG for residue
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; I
DNA 8, 563-574, 1989
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A; Residues: 1-638 < BEA>
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                      A; Accession: I53041
                                               A; Reference number: I53041
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                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A33320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The cDNA structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A39180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A39180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Gene structure and
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                                                                                                                                                                                           A; Accession: S06851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DGSP---
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     GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          of rat plasma kallikrein.
MUID:90091743; PMID:25987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosomal localization of MUID:91129236; PMID:1993180
                                                                        rat
                                                                                                                   Mbikay, M.; Hamelin, J.;
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C;Genetics:
A;Genetics:
A;Gene: PK
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <MAT1>
F;20-109/Domain: apple repeat <AP1>
F;20-109/Domain: apple repeat <AP2>
F;110-199/Domain: apple repeat <AP2>
F;291-380/Domain: apple repeat <AP2>
F;391-638/Product: plasma kallikrein light chain #status experimental <MAT2>
F;391-638/Product: plasma kallikrein light chain #status experimental <MAT2>
F;391-631/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;127,215,308,453,459,494/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;396/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;434,483,578/Active site: His, Asp, Ser #status predicted
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A; Residues: 1-638 <RES>
A; Residues: 1-638 <RES>
A; Cross-references: GB: M58590; NID: g206721; PIDN: AAA42069.1; PID: g206722
C; Comment: This protein, synthesized in the liver, circulates as a noncovalent
C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule
are linked by one or more disulfide bonds.
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                                                                                                                                                                               AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
                                                                                                                                                                                                                                                                                                                       TTKI----NARIVGGTNSSLGEWPWQVSLQVKLVSQNHMCGGSIIGRQWILTAAHCF---D
                                                                                                                                                                                                                                                                                                                                                                  GLRSFTRQARVVGGTDADEGEWPWQVSLHA--LGQGHICGASLISPNWLVSAAHCYIDDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACQETCTKTIRCQFFTYSLLPQDC----KAEGCKC---SLRLST--
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                                             RDYVITKQMICAGYKEGGIDACKGDSGGPL-VCKHSGRWQLVGITSWGEGCARKEQPGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDC-----DC
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                                                                                                                                  LNYTEFOKPICLPSKADTNTIYTNCWVTGWGYTKERGETONILOKATIPLVPNEECOKKY
                                                                                                                                                                                                                          GIPY--PDVWRIYGGILNLSEITNKTP---FSSIKELIIHQKYKMSEGSYDIALIKLQTP
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  TRLPLFRDWIKE
                                                                                       PQQ-ITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVY 667
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27.4%;
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A;Cross-references: UNIPROT:Q03711; EMBL:X59958; NID:g64595; PIDN:CAA42582.1; PID:g64596 C;Superfamily: human complement factor I; LDL receptor ligand-binding repeat homology; tickeywords: hydrolase; serine proteinase F;250-254/Domain: LDL receptor ligand-binding repeat homology <LDL1> F;257-290/Domain: LDL receptor ligand-binding repeat homology <LDL1> F;370-599/Domain: LDL receptor ligand-binding repeat homology <LDL2>
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Mol. Immunol. 30, 1249-1256, 1993
A;Title: Characterization of Xenopus laevis complement factor I structure--conservation
A;Reference number: IS1601; MUID:94019415; PMID:7692240
A;Accession: IS1601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 153; Conserv
                                                                                                                                                  445
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                                                            R-EKGMSRVFHLKWGHINLMD--NCTRVYKERFLDKMECARTYDGSIDACKGDSGGPLVC 561
                                                                                                                                                                                                                                             GIYIGGCWVLTAAHC-----VRSNQPQRYLIMLELLDRLSYDKDLDSFP-----VKSV
                                                                                                                                                                                                                                                                                                                                                                                 GKEDCSDGSDEKDCDCGL-----RSFTROARVVGGTDADEGEWPWQVSLHALGQGHICG
                                                                                                                                                                                                                                                                                                                                                                                                                                 KSEKQEEVEQKQTSEKQEEDLVQESKATQVEEKAKIVNYDIDAERRL----LMKSLPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCDSVNDCGDNSDEQGC-SCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DHSDELNC-----SC----DAGH-QFTCKNKFCKPLFW 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEPGKGIIKVKLPTFEQELFLCGKOWSNREANVVCRQLGSTKGADASASDKVFSLVTEKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPKNATTEVCTDGKRKLQSYCQLKS--VECSNPLNSKYRFSSEAPCTETFTLTQ-----N
            VEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENTG
                                                                                                                                                                                                                                                                                        ASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGL----HDQSQRSAPGVQERRLKRI 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEHCIOATCRGLENSLAECALRKLPMQDNQVAKVTCYTENKDCGFGEFTCSNGKCIPSEL
                                                                                                  HTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGFLSS
                                                                                                                                                    I VHELYNPNTYENDI ALLEVKNI YNNPKCMQADNNMVPACVPWSPFQFKAGDTCTVSGWG
                                                                                                                                                                        ISHPFFNDFTFDYDIALLELB------KPAEYSSMVRPICLPDASHVFPAGKAIWVTGWG
                                                                                                                                                                                                                                                                                                                                        ------LSCGVPPQTAALTLTRKKRVIGGTNAVKNQFPWQVAIKD-GTAVNCG
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Pred. No. 6.2e-26;
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RESULT 11 PLPG plasmin (EC

3.4.21.7)

precursor -

pig

(fragment)

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F;1-77/Domain: plasminogen-related protein precursor homology F;1-77/Domain: activation peptide #status predicted <APT> F;7-8-560/Product: plasmin chain A #status predicted <ACH> F;84-162/Domain: kringle homology <KR1> F;166-243/Domain: kringle homology <KR2> F;156-333/Domain: kringle homology <KR3> F;356-333/Domain: kringle homology <KR3> F;358-345/Domain: kringle homology <KR3> F;358-455/Domain: kringle homology <KR3> F;450-790/Product: miniplasminogen #status experimental <MIN> F;461-540/Domain: kringle homology <KR5>
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C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Compari
A;Reference number: S03733
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Eur. J. Biochem. 149, 279-285, 1985

A;Title: Determination of the complete amino-acid sequence

A;Reference number: A25834; MUID:85203907; PMID:3846533
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R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. Eur. J. Biochem. 114, 465-470, 1981
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Reference number: S03735; MUID:81212097; PMID:7238497
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F;561-783/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
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C; Function:
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A; Residues: 1-57 < BRU>
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A; Accession: A25834
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hes 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAHGYLPSKF-PNKNLKMNYCRN----
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KIPSCGSSTTST----EHL-
                                                                                    ---HSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKE----
                                                                                                                                                                                                                                                                                                                                                                                PTSGPTYQCLKGRGENYRGTVSVTASGHTCQRWSAQSPHKHNRTPENFPCK-NLE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; Score 504; DB 1; Length 790; 25.7%; Pred. No. 1.1e-25; Live 80; Mismatches 238; Indels 2
---DAPVPPEQTPVAQDCYRGNGESYRGTSSTTITGRKCQ 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PDGEPRPWCFTTDPNKRWEFCDIPRCTTPP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SPYYPGHYPPNIDCTWNIEVPNNQ 204
                                                                                                                                                                                        ENYCRNPDGETAPWCYTTDSE---VRWDYC 328
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                                                                                              -----LRCD 300
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A;Molecule type: protein
A;Residues: 118-460 <SC2>
A;Residues: 118-460 <SC2>
A;Residues: 118-460 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z)
F;1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <APT>
F;1-37,58-117,118-230,231-460/Product: plasmin (fragments) #status experimental <APT>
F;38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
F;41-118/Domain: kringle homology <KR4>
F;41-118/Domain: kringle homology <KR4>
F;132-211/Domain: plasmin chain B #status experimental <MIN>
F;236-460/Domain: trypsin homology <KR5>
F;231-453/Domain: trypsin homology <KR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P81286
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Reference number: S28200; MUID:93149995; PMID:1492092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Structural aspects A;Reference number: A61545; A;Accession: B61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: B61545; S28200
R;Schaller, J.; Rickli, E.E
Enzyme 40, 63-69, 1988
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A; Residues: 1-37;38-117 <SCH>
S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmin (EC 3.4.21.7) precursor - N;Alternate names: plasminogen
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                                                                                                                                                                                          ;272,315,410/Active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S28200
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                                                                Matches
                                                                                          Query Match
Best Local
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CGTCPKDYVEINGEKYCGERSQFVV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQ
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                                                                Conservative
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                                                                                          13.3%;
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                                                                                                                                                                                    Asp,
                                                                49;
                                                             Score 503; DB
Pred. No. 7.3e
49; Mismatches
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01-Nov-1996
-TSNSNKITVRFH-SDQSYTDTGFLAEYLSYD
                                                                                          DB 2;
.3e-26;
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#text_change 09-Jul-2004
                                                                                                                       Length 460
                                                                Indels
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serine proteinease stubble-stubbloid (EC 3.4.21.-) - fruit fly (Drosophila melancyspecies: Drosophila melancysaster C; Species: Drosophila melancysaster C; Date: 10.75ep-1999 #sequence_revision 10.75ep-1999 #text_change 09-Jul-2004 C; Accession: A47547 R; Accession: A47547 R; Hammonds, A.; Garbe, J.C.; Fristrom, Proc. Natural R; Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds, A.; Garbe, J.C.; Fristrom, Proc. Natural R; Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds and Stubble Proc. Natural R; Title: The Drosophila Stubble-stubbloid gene encodes an apparent transmembrane A; Reference number: A47547; MUID:93281671; PMID:7685111
                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: FlyBase:FBgn0003319
C;Superfamily: serine proteinease stubb
C;Keywords: hydrolase; serine proteinas
F;61-77/Domain: transmembrane #status p
F;543-781/Domain: trypsin homology <TRY
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A; Residues: 1-786 < APP>
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                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: serine proteinease stubble-stubbloid; trypsin; Keywords: hydrolase; serine proteinase; transmembrane proteinase; transmembrane prote; 51-77/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                                                                                                                                                           Macches
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                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                            C-VDDLLI-----SQIRIRVGEYDFSHVQEQLPYIERGVAKKVV-HPKYSFLTYEYDLAL
                                                                                                                                                                                    CYIDDRGFRYSDPTQWTAFLGLHDQS--QRSAPGVQERRLKRIISHPFFNDFTFDYDIAL
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TCENLL----PQQITPRM-MCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDG
                                                                 VKLEQPLEFAPHVSPICLPETDSLL-IGMNATVTGWGRLSEGGTLPSVLQEVSVPIVSND
                                                                                                    LELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQT
                                                                                                                                                                                                                          ECGVPTLARPETRIVGGKSAAFGRWPWQVSVRRTSFFGFSSTHRCGGALINENWIATAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTDSCQGDSGGPLVCFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSTYVPWIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE--NLLPQQITPRMMCVGFLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYEMAREA-SVOEIPVSRLFLEP-----SRADIALLKLSSPAVITDEVIPACLPSPNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVATPHSWPWQVSLRRRSREHFCGGTLISPEWVLTAAHCLDSILG----PSFYTVILGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --VNGPWCYTTNPRKLFDYC---DIPQCESSFDCGKPKVEPKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE-KDCDCGLRSFTRQARVVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCQE--WAAQEPHRHGIFTPE-----TNPRAGLEKNYCRNPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSDPCPGQFTCRTGRCIRKE----LRCDGWADCTDHSDELNCSCDAGHQFTCKNKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEBEAQDCYHGNGQGYRGTSSTTVTGRKCQSWSSMIPHRHQKTPESYPNAGLTMNYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASC
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                       trypsin homology <TRY>
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                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                            Score 501.5; DB Pred. No. 1.6e-25
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                         89;
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C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflam
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-638/Product: plasma kallikrein #status predicted <MAT>
F;20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F;20-390/Domain: apple repeat <AP2>
F;10-199/Domain: apple repeat <AP2>
F;110-199/Domain: apple repeat <AP3>
F;201-289/Domain: apple repeat <AP3>
F;301-289/Domain: apple repeat <AP4>
F;301-380/Domain: apple repeat <AP4>
F;301-631/Domain: plasma kallikrein light chain #status predicted <LCH>
F;301-621/Domain: trypsin homology <TRY>
F;301-621/Domain: trypsin homology <TRY>
F;31-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein

A;Molecule type: protein

A;Residues: 20-27;40-46,'X',48,'H';50,'X',52-70,'H';75-76,'X',78-80;103-113;131-140;141-1

A;Residues: 20-27;40-46,'X',283-295;314-317,'X',319-320;321-324;'X',329-333;334-339,'X',

525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 <MCMs

C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex will compose the molecule into a light comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a light care linked by one or more disulfide bonds.

C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal reinogen and may also play a role in the renin-angiotensin system by converting prorenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4q35-4q35
C; Superfamily: coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A;Title: Location of the disulfide bonds in human plasma A;Reference number: A37939; MUID:91152016; PMID:1998666
A;Accession: A37939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Chnng, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W. Biochemistry 25, 2410-2417, 1986 A;Title: Human plasma prekallikrein, a zymogen to a serine A;Reference number: A00921; MUID:86243359; PMID:3521732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;127,306,396,453,494/Binding site: carbohydrate (Asn) (cover;318-347,540-345/Disulfide bonds: #status predicted F;318-347,Cleavage site: Arg-Ile (coagulation factor XIIa) F;434,483,578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GDB:127575; OMIM:229000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasma kallikrein
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R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-638 <CHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Homo sapiens (man)
;Date: 13-Aug-1986 #sequence_revision
;Accession: A00921; A37939
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                         154
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                                                                                                                                                                                                         GF--EATFFOLPR-----MSSCGGRLRKAQGTFNSPYYPGHYPPNID-----
SVEECOKRCTNNIRC---OFFSYATOTFHKAEYRNNCLL
                                                                 ----CTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYC--GERSQ 243
                                                                                                                                                                                                                                                                          RGGDVASMYT-----PNA--QYC----QMRCTFH--PRCLLFSFLPASSINDMEKRFG
                                                                                                                                                                                                                                                                                                                                                RGSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITL-----ITNTERRHP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCKSMFMRAGRQEFIPDIFLCAGYETGGQDSCQGDSGGPLQAKSQDGRFFLAGIISWGIG 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 499; DB 1;
Pred. No. 1.9e-25;
2; Mismatches 212
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                                                                                                                                   -SACHRDI YKGVDMRGVNFNVSKVS
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                                                                                                                                                                                                                                                                                                                                                                                                                         231;
KYSPGGTPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
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complement factor I (EC 3.4.21.45) precursor - human
N.Alternate names: C3b/C4b inactivator
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #text_change 09-Jul-2
C;Accession: A29154; A28434; $66420
R;Catterall, C.F.; Lyons, A.; Sim, R.B.; Day, A.J.; Harris, T.J.R.
Blochem. J. 242, 849-856, 1987
A;Title: Characterization of the primary amino acid sequence of human cc
A;Reference number: A29154; MUID:87241401; PMID:2954545
A;Accession: A29154
A;Residues: 1-583 <CAT>
A;Residues: 1-583 <CAT>
A;Caross-references: UNIPROT:P05156; GB:Y00318
R;Goldberger, G.; Bruns, G.A.P.; Rits, M.; Edge, M.D.; Kwiatkowski, D.J.
J. Biol. Chem. 262, 10065-10071, 1987
A;Fitle: Human complement factor I: analysis of cDNA-derived primary str
A;Reference number: A28434; MUID:87280021; PMID:2956252
A;Accession: A28434
A.MClocassion: A28434
                                                                                                                                 A)ACCESSION: S66*20
A;Molecule type: protein
~ masidues: 258-269 (ULL)
A;Gene: GDB:IF
A;Cross-references: GDB:120077; OMIM:217030
A;Map position: 4q24-4q25
C;Superfamily: human complement factor I; LE
C;Keywords: glycoprotein; hydrolase; serine
                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Rosidues: 1-557,'F',559-583 <GOL>
A;Residues: 1-557,'F',559-583 <GOL>
A;Cross references: GB:J02770; NID:g182606; PIDN:AAA52455.1; PID:g182607
A;Closs references: GB:J02770; NID:g182606; PIDN:AAA52455.1; PID:g182607
A;Ullman, C.G.; Haris, P.I.; Smith, K.F.; Sim, R.B.; Emery, V.C.; Perkin:
R;BBS Lett. 371, 199-203, 1995
A;Title: beta-Sheet secondary structure of an LDL receptor domain from co
A;Reference number: S66420; MUID:95402210; PMID:7672128
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                                                                                                                         A;Residues:
C;Genetics:
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                            LDL receptor ligand-binding repeat homology;
     proteinase
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                                                                            QRNKPGVYTRLPLFRDWIKENTG
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KPEFPGVYTKVANYFDWISYHVG
                                                                                                                                                        -SNCSKFYGNRFYEKEMECAGTYDGSIDACKGDSGGPLVCMDANNVTYVWGVVSWGENCG
                                                                                                                                                                                                                                        QTTCENLLPQQITPR-MMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCA
                                                                                                                                                                                                                                                                                                                        MKKDGNKKDCELPRSIPACVPWSPYLFQPNDTCIVSGWGR-EKDNERVFSLQWGEVKLI-
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plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627;
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
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A;Title: Characterization of the gene for human plasminogen, a key proenzyme
A;Reference number: A35229; MUID:90202879; PMID:2318848 A;Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; GB:J05286; GB:M34276; A;Experimental source: leukocyte; lung fibroblast R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Taz Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene in live Reference number: 152242; MUID:91097523; PMID:2268308 A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613 R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O. FEBS Lett. 213, 254-260, 1987 A; Molecule type: DNA A; Residues: 1-16 < MAL1> A; Molecule type: DNA A; Residues: 1-810 < PET> A; Accession: I52242 A; Accession: A35229 Status: translated from GB/EMBL/DDB

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A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
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A; Residues: 20-71, 'E', '73-76 < BRU>
R; Sottrup-Jensen, L; Petersen, T.E.; Magnusson, submitted to the Atlas, July 1977
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R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria,
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A;Accession: A04625
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A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1;
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                                                                                           R;Trexler, M.; Vali, Z.; Patthy, L.
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A;Reference number: A92382; MUID:82213905; PMID:6319539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <WI2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Structural relationship
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 581-810 <WI1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
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A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Malinowski, D.P.; Sadler, J.E.; Davie, Biochemistry 23, 4243-4250, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental
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A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                          Contents: annotation; active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Residues: 367-419 <MAL3>
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                                                            Contents: annotation; omega-aminocarboxylic acid binding sites
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13690-13694, 1984
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Ride Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.J. Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
A;Reference number: A39433; MUID:92118803; PMID:1310033
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wu, T.P.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank, A;Reference number: A51911; PDB:1PKR
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                                                                                                    R;Rejante, M.R.; Llinas, M. Eur. J. Biochem. 221, 927-937, 1994
                                                                                                                                                                    A; Reference number: A65804; PDB:1HPK A; Contents: annotation; conformation
                                                                                                                                                                                                                                    A;Contents: annotation; conformation by (R;Rejante, M.; Llinas, M. submitted to the Brookhaven Protein Data
                                                                                                                                                                                                                                                                                                                                         submitted to the Brookhaven Protein Data Bank, August 1996
A,Reference number: A65803; PDB:1HPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KRN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Contents: annotation; X-ray crystallography, R;Padmanabhan, K.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Brookhaven Protein Data Bank,
A;Reference number: A51488; PDB:2PK4
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A;Title: (1)H-NMR assignments and secondary structure of human plasminogen A;Reference number: S43645; MUID:94237157; PMID:8181475 A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
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A;Reference number: A65244; PDB:1CEA
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A;Reference number: A58812; MUID:9548733; PMID:9548733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contents: annotation, (?) Tulinsky, A.; Mulichak, A.M.
(;) Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
(iochemistry 30, 10589-10594, 1991
(;) Title: The refined structure of the epsilon-aminocaproic
(;) Title: The refined structure of the epsilon-aminocaproic
(;) Reference number: A58818; MUID:92031503; PMID:1657149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Contents: annotation; X-ray crystallography,;Tulinsky, A.; Mathews, I.I.
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                                                                                                                                                                                                                                                                                                                                                                                                                Rejante, M.; Llinas, M.
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linsky, A.; Mathews, I.I.
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                                                                                                                                                                                                                                                                                                            conformation by (1) H-NMR, residues
                                                                                                                                                                           by (1) H-NMR,
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R; Rejante, M.R.; Llinas, M.

J. Biochem. 221, 939-949, 1994 tle: Solution structure of the epsilon-aminohexanoic ference number: A58817; MUID:94237158; PMID:8181476

acid

complex

of human

plasminog

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A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein
C;Superfamily: plasmin; kringle homology; duplication; fibrinolysis;
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-96/Domain: signal sequence #status predicted <SIG>
F;20-810/Product: plasminogen #status experimental <PRO>
F;20-96/Domain: activation peptide #status experimental <AST>
F;79-466/Product: angiostatin #status experimental <AST>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;97-580,581-810/Product: plasmin #status experimental <MAT:
F;97-580/Domain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR4>
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C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately aff c:Comment: Plasmin is inactivated by two disulfide bonds. Without the inhibitor, rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor, C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial cond C:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: dissolves the ns the walls of the graafian
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A; Introns: 17/1; 62/2; 98
C; Function:
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C;Comment: Plasminogen is synthesized by the kidney and is present in plasma
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see
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A;Cross-references: GDB:119498; OMIM:173350
                                                                                                                                                                                                                                                                366
                                                                                                                                                                                                                                                                                                                    410
                                                                                                                                                                                                                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                                                                                                                                                          366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                 VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTA
                                                                                                                                                                                                                                                                                                                                                                      QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSC----PAQTFR-CSNGKC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYCRNPDGKRAPWCHTTNSQ---VRW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NYRGNVAVTVSGHTCQHWSAQTPHTHN------RTPENFPCKNLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGHYPPNIDCT-----WNIEVPNNOHVKVRFKFFYLLEPRRACGTCPKDYVEIN-GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCRN----PDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLKGTGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSONVLLITLITHTERR-----HPGFEATFFOLPRMS----SCGGRLRKAQGTFNSPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLASCDER-----GSDL-VTVYNTLSPME-----PHALVQLCGTYP---PSYNLTFH 134
VVGGCVAHPHSWPWQVSLRTRFGMHFCGGTI
                                                                                                      GLEKNY-CRNPDG----DVGGPWCYTTNPRKLYDYCDVPQCAAPSFDCGKPQVEPKKCPGR
                                                                                                                                                          CTKHTYRCLN--GLCLSKGNPEC--DGKEDCSDGSDEKDC----
                                                                                                                                                                                                              PPVVLLPNVETPSEEDCMFGNGKGYRGKRATTVTGTPCQDWAAQEPHRHSIFTPETNPRA
                                                                                                                                                                                                                                                             ----LSKSQQCNGKDDC--GDG------SDEAS------CPKVNVVT
                                                                                                                                                                                                                                                                                                                       QKTPENYPNAGL-----TMNYCRNPDADKGPWCFTTDPSVRWEYCNLKKCSGTEASVVAP
                                                                                                                                                                                                                                                                                                                                                                                                                          APPELTPVVQDCYHGDGQSYRGTSSTTTTGK-----KCQSWSSMTPHR------H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILECEBECMHCSGENYDGKISKTMSGLECQAWDSQSPHA----HGYIPSKFPNKNLKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98/1; 136/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 492.5; 27.0%; Pred. No. 6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibrin of blood clots; acts as a proteolytic follicle; also activates the urokinase-type p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GQ-----FTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EYCKIPSCDSSPVSTEQLAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elated protein precursor homology
fibrinolysis; glycoprotein; hydr
                                                                                                                                                       -DCGLRSFTRQ---AR
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  PSSYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasminogen
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A;Cross-references: UNIPROT:P20918; GB:J04766; NID:g200402; PIDN:AAA50168.1; R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D. Bur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system. A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmin (EC 3.4.21.7) precursor - mouse
NyContains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change
C;Accession: A38514; S48202; $\overline{5}{2}48203$
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics B, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminog
A;Reference number: A38514; MUID:91184812; PMID:2081600
                                                                                                                                                                                 F;97-581/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;105-262/Domain: kringle homology <KR2>
F;185-262/Domain: kringle homology <KR3>
F;275-352/Domain: kringle homology <KR4>
F;377-454/Domain: kringle homology <KR4>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-812/Domain: trypsin homology <TRY>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,324
Donds: #status predicted
Donds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminogen-related
C; Superfamily: plasmin; kringle homology; duplication; fibrin
C; Keywords: angiogenesis inhibitor; blood; duplication; fibrin
F;1-96/Domain: plasminogen-related protein precursor homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-81/Product: plasminogen #status predicted <APT>
F;20-96/Domain: activation paptide #status predicted <APT>
F;79-466/Product: angiostatin #status predicted <AST>
F;97-581,582-812/Product: plasmin #status predicted <AMT>
F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental F;524-667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: Stromelysin 1 (see PIR:KCMSS1)
eful in treating solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin mediately after dissociation from the clot. In the presence of the inhibitor, the activate e inhibitor, the activation involves also removal of the activation peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: dissolves the fibrin of blood clots; acts as a proteolytic ns the walls of the graafian follicle; also activates the urokinase-type [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues:
C;Comment: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 22-27 <LI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 20-25 < LIJ >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-812 < DEG>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A14757; B20274; T45891; A00923
R;Katayama, K.; Ericeson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A;Title: Comparison of amino acid sequence of bovine coagulation factor IX (Chri A;Reference number: A14757; MUID:80056619; PMID:291916
A;Accession: A14757
A;Rocession: A14757
A;Residues: 1-63,'T',65-416 <KAT>
A;Rocess-references: UNIPROT:P00741
R;MCMullen, B.A.; Fujikawa, K.; Kisiel, W.
                                                                                                                                                                                                                                                          RESULT 18
KFBO
                                                                                                                                                                                                                      coagulation factor IXa (EC 3.4.21.22) precursor - N_iAlternate names: Christmas factor
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Best Local S
Matches 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHOFTCKNKFCKPLFWVCDSVNDC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVEINGEKYCGERSQFVVTSNSNKITVRF---HS--DQSYTDTGFLAEYLSYDSSDPCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIPRCTTPPPPPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENL--LPQQITPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFYKVILGAHEEYIRGL-DVQEISVAKLILEP----NNRDIALLKLSRPATITDKVIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQARVVGGTDADEGEWPWQVSLHALGQG-HICGASLISPNWLVSAAHCYIDDRGFRYSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYT--TDPSVR-----WEYC----NLKRCSETGGSVVELPTVSQEP-SGPSDSETDCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WNIEV-----PNNOHV------KVRFKFFYL-----LEPRRACGTCP------KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SPHA----HGYIPAKFPSKNLKMNYCHN-----PDGEPRPWCFTTDPTKRWEYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPMEPHALVQLCGTYP---PSYNLTFHSSQNVLLITLITNTERR-----HPGFEATFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTTD--PDKRYDYCNIPECEEECMYCSGEKYEGKISKTMSGLDCQAWDSQ------
                                                                                                                                                                                                                                                                                                                                                                      WIK 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - PGRVVGGCVANPHSWPWQISLRTRFTGQHFCGGTLIAPEWVLTAAHCL----EKSSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EASCPKVNVVTCTKHTYR-----CLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGNGKDYRGKTAVTAAGTPCQGWAAQEPHRHSIFTPQTNPRADLEKNYCRNPD--GD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GDNSDEQG-----CSCPAQTFRC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NLEENYCRNPDGETAPWCYTTDSQLRWEYCEIPSCESSASPDQSDSSVPPEEQTPVVQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 491.5; DB 1;
Pred. No. 7.4e-25;
4; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GTFGAGRIKEAQLPVIENKVCNRVEYLNNRVKST
                                                                                                                                                                                                                                            bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGKCLSKSQQCNGKDDCGDGSD
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A; Residues: 52-139 < CHO>
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Best Local Similarity
                        565
                                                                                                                                  191
                                                                                                                                                                                                                                                                              101
                                                                                                                                                                  452
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A;Description: catalyzes the proteolytic activation of coagulation factor X in the present A;Pathway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Reywords: beta-hydroxysapartic acid; blood coagulation; calcium binding; carboxyglutam:
F;1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
F;1-45/Domain: Gla domain homology (fragment) <GLA>
F;51-82/Domain: EGF homology <EGI>
F;147-181/Domain: EGF homology <EGI>
F;147-181/Domain: activation peptide #status experimental <APT>
F;182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;182-4409/Domain: trypsin homology <TRY>
F;182-4409/Domain: trypsin homology <TRY>
F;18-23/Sinding site: carbohydrate (Ser) (covalent) #status experimental
F;64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;222,270,386/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A; Title: The occurrence of beta-hydroxyaspartic acid in the A; Reference number: A20274; MUID:83308813; PMID:6688526

A; Accession: B20274

A; Molecule type: protein

A; Residues: 59-63, 'X', 65-69 < MCM>

R; Choo, K. H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.

Nature 299, 178-180, 1982

A; Title: Molecular cloning of the gene for human anti-haemo A; Reference number: 145891; MUID:82272386; PMID:6287289

A; Accession: 145891

A; Status: translated from GB/EMBL/DDBJ
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R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga
J. Biochem: 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood co
A;Reference number: AA4556; MUID:89213999; PMID:3149637
A;Contents: annotation
A;Wote: structure and location of a carbohydrate covalently bound to Ser
C;Comment: Factor IX is activated by factor XIa, which excises the activational, vitamin C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with st
C;Function:
EEFVRGNLERECKEEK-----CSFEEAREVFENTEKTTE--FWKQYVDGDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDYVEINGEKYCGERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                SHISKKLTRA--ETIFSNTNYENSSEAEIIWDNVTQSN----QSFDEFSRVVGGEDAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTCTKHTYRCLNGLCLSKGNPECDGK-EDCSDGSDEKDCDCGLRSFTRQARVVGGTDADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNV
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                                                                                                                                                                                                                                                                                                                                                       GEWPWQVSLHALGQGHI----CGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHD
                                                                                                                                                                                             OSORSAPGVOERRIKRIISHPFFNDF--TFDYDIALLELEKPAEYSSMVRPICIPDA--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RDTDNKVVCS-----CTDGYRLAEDQK-----SC-EPAVPFPCGRVSV
                                                                                                                     -TEKPEPTEQKRNVIRAIPYHSYNASINKYSHDIALLELDEPLELNSYVTPICIADRDYT
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29.1%;
                                                                                                                                                                                                                                                                          -GEIAAFCGGSIVNEKWVVTAAHC-----IKPGVKITVVAGEHN
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Pred. No. 4.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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C;Species: Homo sapi
C;Date: 31-Dec-1988:
C;Accession: S00845
R;Leytus, S.P.; Loeb
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A;Cross-references: GDB:135685; OMIM:142440
A;Map position: 19q11-19q13.2
C;Superfamily: trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: transmembrane #status predicted <TMN>
F;163-400/Domain: trypsin homology <TRY>
F;163-400/Domain: trypsin homology <TRY>
F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F;203,257,353/Active site: His, Asp, Ser #status predicted
                C;Accession: A57014; A54866
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A;Title: Molecular cloning, tissue-specific
A;Reference number: A57014; MUID:95286644; E
A;Accession: A57014
                                                                                                                                                                                               RESULT
A57014
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A;Title: A novel trypsin-like serine protease (hepsin) with a A;Reference number: $00845; MUID:88209431; PMID:2835076
A;Accession: $00845
                                                                                                           prostasin (EC 3.4.21.-) precursor - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996
C;Accession: A57014; A54866
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A;Cross-references: UNIPROT:P05981;
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Best Local
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                                                                                                                                                                                                                                                                          VDSCQGDSGGPL---SSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWI
                                                                                                                                                                                                                                                                                                                                                     VDGKI CTVTGWGNTQYYGQQAGVLQEARVPI I SNDVCNGADFYGNQI KPKMFCAGYPEGG
                                                                                                                                                                                                                                                                                                                                                                                          PAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE--NLLPQQITPRWMCVGFLSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APGVQERRLKRIISH----PFF--NDFTFDYDIALLELEKPABYSSMVRPICLPDASHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKHTYRCLNGLCLSKGNPECDGKEDCSDGSD-EKDC-DCGLRSFTRQARVVGGTDADEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGDNSDEQ--GCSCPAQTF--RCSNGKCLSKSQQCNGKDD--CGDGSDEASCPKVNVVTC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENT 681
                                                                                                                                                                                                                                                                                                                                                                                                                                   PHGLQ-LGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPWQVSLRYDG-AHLCGGSLLSGDWVLTAAHCFPE----RNRVLSRWRVFAGA--VAQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSSRSNARVAGLSCEEMGFLRALTHSELDVRTAGANGTSGFFC---VDEGRLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKDSCQGDSGGP-HVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRYVNWIKEKT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIFSKFGYGYVSGWGKVFNRGRSASILQYLKVPLVDRATCLRSTKFSIYSHMFCAGYHEG 357
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from
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    GB/EMBL/DDBJ
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                                      PMID:7768952
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                                                                                                                                  #text_change
                                                           and
                                                           cellular localization
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coagulation factor IXa (BC 3.4.21.22) precursor [validated] - human N,Alternate names antihemophilic factor B; Christmas factor C;Species: Homo sapiens (man) C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004 C;Accession: A00922; A37570; Ā30511; A32989; A22673; A21337; A37546; A30623; R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, B.W.; Kurachi, K. Biochemistry 24, 3736-3750, 1985
Biochemistry 24, 3736-3750, 1985
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic A;Reference number: A00922; MUID:86000558; PMID:2994716
EMBO J. 3, 1053-1060, 1984
A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; MUID:84236100; PMID:6329734
A;Accession: A37570
                                                                                 A;Cross-references: UNIPROT:P00740; GB:K02402; NID:g182612; R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Goul EMBO J. 3, 1053-1060, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;33-44,45-343/Product: prostasin #status predicted <MAT>
F;33-44/Domain: prostasin light chain #status predicted <CHL>
F;35-943/Domain: prostasin heavy chain #status predicted <CHH>
F;45-943/Domain: trypsin homology <TRY>
F;45-281/Domain: trypsin homology <TRY>
F;323-341/Domain: transmembrane #status predicted <TMM1>
F;37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
F;85,134,238/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: parts of this sequence were determined by protein sequencing R;Yu, J.X.; Chao, L.; Chao, J.
B;Ol. Chem. 269, 18843-18848, 1994
A;Title: Prostasin is a novel human serine proteinase from seminal fluid.
A;Reference number: A54866; MUID:94308140; PMID:8034638
                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-461 < YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;85,134,238/Active site: His, Asp, Ser #status predicted F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                        A; Accession: A00922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDACQGDSGGPL-SCPVEGLWYLTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQTTCENLL-----PQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAEGAEAPCGV---APQARITGGSSAVAGQWPWQVSITYEGV-HVCGGSLVSEQWVLSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSWGDACGARNRPGVYTLASSYASWIQ
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39.3%; Pred. No. 9.1e-25;
tive 42; Mismatches 95
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                                                                                                                    612; PIDN:AAB59620.1; PID:g182613 Gould, K.; Huddleston, J.A.; Brov
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A; Molecule type: mRNA
A; Residues: 1-193,'T','195-461 <MCG>
A; Residues: 1-193,'T','195-461 <MCG>
A; Residues: 1-193,'T','195-461 <MCG>
A; Residues: 1-193,'T','195-461 <MCG>
A; Rote: the authors translated the codon ACA for residue 29 as Tyr
A; Note: the authors translated the codon ACA for residue 29 as Tyr
R; Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstosh
Ruccleic Acids Res. 11, 2325-2335, 193
R; Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A; Reference number: A21337; MUID:83220788; PMID:6687940
A; Accession: A21337; MUID:83220788; PMID:6687940
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                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 47-52, XX', 55-60,'X', 62,'XX', 65 <THA>
A;Residues: 47-52, XX', 55-60,'X', 62,'XX', 65 <THA>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
B;Tile: The occurrence of beta-hydroxyaspartic acid in the A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Recession: A20274
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Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A;Title: Isolation and characterization of a cDNA coding A;Reference number: A30623; MUID:83065193; PMID:6959130
A;Accession: A30623
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A;Cross-references: GB:J0013; D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
R;Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A;Title: Isolation and characterization of human factor IX cDNA: identif.
A;Reference number: A37546; MUID:84300526; PMID:6089357
A;Accession: A37546
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R;RCGTAW, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A;Reference number: A22673; MUID:85190593; PMID:3857619
A;Accession: A22673
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A;Title: The putative factor IX gene promoter in hemophilia B
A;Reference number: A30511; MUID:88327116; PMID:3416069
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A;Residues: 38-193,'T',195-326 <JAG>
A;Cross-references: GB.M35672
                                                                                                                                                         A; Molecule type: protein
A; Residues: 105-109, 'X', 111-115 < MCM>
R; Balland, A.; Faure, T.; Carvallo, D.;
Eur J. Biochem. 172, 565-572, 1988
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A;Title: Development of an immunoaffinity process for factor IX property of the process for factor IX proc
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A;Residues: 1-12,'S',14-73,'P',75-82,'K',84-203,'P',205-216,'G',218-298,'A',299-356,'A'
A;Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
A;Experimental source: liver
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A; Residues: 8-24 < REI>
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JTitle: Characterisation of two differently processed forms; Reference number: S02527; MUID:88166735; PMID:3280312; Accession: S02527
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R; Morita, T; IBaacs, B.S; Esmon, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A; Title: Derivatives of blood coagulation factor IX contain a h.
A; Reference number: A37543; MUID:84185715; PMID:6425296
A; Contents: annotation; Calcium binding
R; Morita, T; IBaacs, B.S.; Esmon, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A; Reference number: A37544
A; Contents: annotation; Calcium binding, correction
A; Contents: annotation; Calcium binding, correction
A; Contents: annotation; Calcium binding, Correction
A; Ference number: A37545; MUID:86189947; PMID:3009023
A; Contents: annotation; Signal sequence cleavage site
R; Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamats
J. Biol. Chem. 264, 21257-21265, 1989
A; Title: Blood clotting factor IX B(M) Nagoya: substitution of a h; Contents: A3622; MUID:90078229; PMID:2592373
A; Contents: A3622; MUID:90078229; PMID:2592373
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A, Molecule type: protein

A, Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' < AGA>

A, Note: the residues designated 'X' were determined to be threonine bour

R, Di Scipio, R. G.; Kurachi, K.; Davie, E.W.

J. Clin. Invest. 61, 1528-1538, 1978

A, Title: Activation of human factor IX (Christmas factor).

A, Reference number: A18483, MUID:78194509; PMID:659613

A, Contents: annotation; activation; active site; carbohydrate binding

R, McGraw, R. A.; Davis, L. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, L. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Graham, J. B.; Roberts, H. R.; 'RMCGraw, R. A.; Davis, C. M.; Noyes, C. M.; Noyes,
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A;Title: Activation peptide of human factor IX has oligosaccharides O-gly A;Reference number: A54255; MUID:94227047; PMID:8172892
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A;Title: Genomic amplification with transcript sequencing A;Reference number: 159529; MUID:88127096; PMID:3340835
A;Accession: 159529
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R;Title: A deletion located in the 3' non translated part of A;Reference number: I59612; MUID:94054330; PMID:8236150

A;Accession: I59612
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A;Title: The first EGF-like domain from human factor IX conta: A;Reference number: S12377; MUID:90151623; PMID:2406129
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A;Title: Characterization of recombinant human Factor IX
A;Reference number: S12058; MUID:91006024; PMID:2209546
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A;Cross-references: GB:S66752; NID:g439773;
R;Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.;
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A;Residues: 290-359 <RE2>
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A; Residues: 92-130 < HAN>
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A; Molecule type: pro
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A; Gene (GDB:F9)
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A; Gene (GDB:F9)
A; Gene (GDB:F9)
A; Cross-references: GDB:119900; OMIM:306900
A; Map position: Xq27,1-Xq27.2
A; Introns: 30/1; 84/2; 93/1; 13/1; 174/1; 241/3; 280/1
C; Function:
A; Description: catalyzes the proteolytic activation of coagulation factor X in the prese A; Pathway: blood coagulation intrinsic pathway
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Seywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-28/Domain: signal sequence #status predicted <SIG>
F;2-191/Domain: Gla domain homology <GGL>
F;2-191/Domain: Gla domain homology <GGL>
F;31-91/Domain: Gla domain homology <GGL>
F;47-191/Product: coagulation factor IXa light chain #status experimental <APP>
F;47-191/Domain: EGF homology <EGL>
F;134-170/Domain: activation peptide #status experimental <ACT>
F;227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;227-461/Product: coagulation peptide #status experimental <ACT>
F;227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;23,54,61,63,66,772,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #sfides site: carbohydrate (Ser) (covalent) #status experimental
F;203,213/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;203,213/Binding site: carbohydrate (Man) (covalent) #status experimental
F;205-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental
F;206-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental
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A;Note: recombinant form expressed in yeast
C;Comment: Factor IX is activated by factor XIa, which excises the activation processed in yeast
C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational,
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and,
C;Genetics:
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R;Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.;
submitted to the Brookhaven Protein Data Bank, November 1991
A;Reference number: A51252; PDB:1IXA
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                                                                                                                                                                                                        KRIISHPFFNDF--TFDYDIALLELEKPAEYSSMVRPICLPDASHV-----FPAGKAIWV
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                                 SGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQGDSGG
                                                                                                                                                 IRII PHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADKEYTNIFLKFGSG----YV
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Pred. No. 1.2e-24;
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plasmin (EC :
C;Species: E:
C;Date: 21-Fe
C;Accession:
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A;Title: The recurring evolution of Lp(a): Insights from cloning A;Reference number: I46259; MUID:96025778; PMID:7592597
A;Accession: I46260
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                                                                                                                                                                                                                                                                                                                                                         DYCDIPHCVSPSS----ADCG-----KPKVEPKKCPGRVGGCVAHPHSWPWQVSLRRFG
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                                                                                                                                                                         IISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGPWCYTTDPSVRWEFCNLKKCSGTEMSATNSSPVQVSSASESSEQDCIIDNGKGYRGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QECYQGNGQTYRGTSSTTITGKKCQP---WTSMRPHRHSKTPENYPDADLTMNYCRNPDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNCSCDAGHQF-----TCKNKFCKPLFWV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LECOPWDSQIPHPHGFIPSKFPSKNLKMNYCRNPDGEPRPWCFTMDRNKRWEYCDIPRCT
   TYGAGLLKEAQLPVIENKVCNRQSFLNGRVRSTELCAGHLAGGVDSCQGDSGGPLVCFEK
                                                                                                                   MFLEP----YRADIALLKLSSPAIITDKDHPACLPNSNYMVADRSLCYITGWGETK-G
                                                                                                                                                                                                                                      Q-HFCGGTLISPEWVVTAAHCL-----EKFSNPAIYKVVLGAH-QETRLERDVQIKGVTK
                                                                                                                                                                                                                                                                                                                                                                                                                --CDGKEDCSDGSDEKDCDCGLRSFTRQARV-----VGGTDADEGEWPWQVSLHALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGAGTPCQAWAAQEPHRHSIFTPETNPRADLQENY-CRNPDGDANGPWCYTTNPRKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGCSC----PAQTFR-CSNGKCL------SKSQQC---NGKDDCGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLAEYLSYDSSDPCPGQFTCRTGRCIRKEL----RCDGWADCTDHSDE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPPPSGPTYOCLMGNGEHYQGN-----VAVTVSGLTCQRWGEQSPHRHDRTPENYPCKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROT:Q29485; EMBL:U33171; NID:g1046360; PID:g1046361
kringle homology; plasminogen-related protein precu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%;
26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NGEKYCGERSQFVVTSNSNKITVRFHSDQS-----YTDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----CPKVNVVTCTKHTYRC----LNGLCLSKGNPE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 483; DB 2;
Pred. No. 2.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TNSSVRWEFCKIPDCVSSASETEHSDAPVIVPPEQTPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CD-SVNDCGDNSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor homology;
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769 642 709 656 524 603 464 553 414 494 381 434

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A;Cross-references: UNIPROT:P06868; EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g49494, RExperimental source: liver
A;Rote: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J: Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick Bur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasm A;Reference number: A25835; MUID:85203906; PMID:3846532
A;Accession: A25835
                                                                                                                                                                                                                                                                                                                                                                                                          F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <AMT>
F;104-583/Domain: plasmin chain A #status experimental <ACH>
F;110-188/Domain: kringle homology <KR1>
F;110-269/Domain: kringle homology <KR2>
F;192-269/Domain: kringle homology <KR3>
F;282-359/Domain: kringle homology <KR3>
F;384-612/Domain: kringle homology <KR3>
F;384-612/Domain: kringle homology <KR4>
F;384-612/Domain: kringle homology <KR5-
F;384-612/Domain: plasmin chain B #status experimental <BCH>
F;584-812/Domain: plasmin chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Superfamily: plasmin; kringle homology; plasminogen-related protein c;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidne: F;1-26/Domain: signal sequence #status predicted cSIG-F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>F;27-812/Product: plasminogen #status experimental <PRO>F;27-812/Product: plasminogen #status experime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 27-334, D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
R; Malinowski, D.F.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
B; Title: Characterization of a complementary deoxyribonucleic A; Reference number: 145961; MUID:85023311; PMID:6148961
A; Accession: 145961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence revision 28-Apr-1995
C;Accession: S45046; A25835; T45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A;Description: Cloning and characterizatin of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mannebe Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of A;Reference number: S03735; MUID:81212097; PMID:7238497
                                                                                                                                                                                                                                                                                                            F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor ns the walls of the graafian follicle; also activates the urokinase-type plasmind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: F
A; Residues: 27-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Pathway: fibrinolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S03736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 706-743, 'R', 745-812 <MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S45046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmin (EC 3.4.21.7) precursor -
N;Alternate names: plasminogen
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                                                                                                                                /Binding site: carbohydrate (Asn)
/Binding site: carbohydrate (Ser)
,667,762/Active site: His, Asp, Se
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                    #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE
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12.7%;
27.3%;
Score
Pred.
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                                                                                                                                     (covalent) #status experimental (covalent) #status experimental ar #status predicted
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481.5; DB 1;
No. 3.4e-24;
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Lergier, W.;
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e; kidney; kringle; plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change
C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution,
A;Reference number: A32869; MUID:89174660; PMID:2925643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmin (EC 3.4.21.7) precursor - rhesus macaque C;Species: Macaca mulatta (rhesus macaque) C;Date: 31-Mar-1989 #sequence_revision 31-Mar-198 C;Accession: B32869; B30848
                                         F;103-181/Domain: kringle homology <KR1>
F;185-62/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
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                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
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F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,324
                                                                                                                                                               F;1-96/Domain: plasminogen-related pro
F;1-9/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                                                                       A; Accession: B32869
                                                                                                                                                                                                           Superfamily: plasmin; kringle homology; plasminogen-related protein precursor; keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
                                                                                                                                                                                                                                                                                  Residues: 1-810 <TOM>
                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                 Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDVPVPPEQT--PVPQDCYHGNGQSYRGTSSTTITGRKCQSWSSMTPHRHLKTPENYPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LEPRRACGTCPKDYVEINGEKYCGERSQFVV---TSNSNKITVRFH--SDQSYTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVRVSPYVPWIEE 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLDGRVKPTELCAGHLIGGTDSCQGDSGGPLVCFEKDKYILQ-GVTSWGLGCARPNKPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTC--EN 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILALSF-----YKVILGAHNEKVRE-QSVQEIPVSRLFREP-----SQADIALLKLSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGTGKSYRGKKATTVAGVPCQE--WAAQEPHQHSIFTPB---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDAGHOFTCKNKF-----CKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKS 369
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                                                                                                                                                               predicted <SIG>
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                                                                                                                                                                                          homology
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F;622,665,760/Active site: His,

Asp,

Ser #status predicted

Score 481;

DB 2;

Length 810,

<u> </u>	QY 431 DCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDR 490
0,	Query Match 12.7%; Score 480.5; DB 1; Length 416; Best Local Similarity 38.6%; Pred. No. 2e-24; Matches 105; Conservative 42; Mismatches 96; Indels 29; Gaps 10
PID:957929	A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-416 <far> A; Cross-references: UNIPROT:Q05511; EMBL:X70900; NID:g57928; PIDN:CAA50256.1; A; Cross-references: UNIPROT:Q05511; EMBL:X70900; NID:g57928; PIDN:CAA50256.1; C; Superfamily: trypsin homology C; Keywords: hydrolase; liver; serine proteinase; transmembrane protein F; 22-44 / Domain: transmembrane #status predicted <tmn> F; 18-49 / Domain: trypsin homology <try> F; 187-203,290-358,321-337,348-380 / Disulfide bonds: #status predicted F; 202,256,352 / Active site: His, Asp, Ser #status predicted</try></tmn></far>
proteinase.	<pre>vegicus (Norway rat) sequence revision 06-Jan-1995 #text_change 16-Aug-2004 Sequence revision 06-Jan-1995 #text_change 16-Aug-2004 S32013</pre>
	RESULT 25 S33777
	Db 799 FVTWIE 804
	Qy 673 FRDWIK 678
80 N	Qy 613 TPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPL 672
	Db 681 VIPACLPSPNYVVADRTECFITGWGETQ-GTYGAGLLKGARLPVIENKVCNRYEFLNGTV 739
	628 SRPSFYKVILGAH-REVHLEPHVQEIEVSKMFSEPARADIALLKLSSPAIITDK
-44	SHPFFNDFT
7	573 EPKKCPGRVVGGCVAYPHSWPWQISLRTRLGWHFCGGTLISPEWVLTAAHCLEKS
	DD 513 HRIFTPETNPKAGLEKNYCKNPDGDVGGPWCYTTNPKKLFDYCDVPQCAASSFDCGKPQV 572 OV 438 TROARVVGGTDADEGEWDWOVSLHALGOGHICGASLISDNWLVSAAHCYIDDRGFRY 494
7	400 YRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSF
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	316 CDAGHQETCKNKECKELEWVCDSVNDCGDNSDEQGCSCPAQTERCSNGKCLSKSQQ
7 5	QY 257 FHSD-QSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCS 315
7 6	Db 321 ENYCRNPDGEKAPWCYTTNSQVRWEYCKIPSCESSPVSTEPLDPTAPPELTPVVQEC 377
	Best Local Similarity 29.1%; Pred. No. 3.6e-24; Matches 159; Conservative 54; Mismatches 169; Indels 164; Gaps

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A;Cross-references: GDB:119891; OMIM:264900
A;Map position: 4q35-4q35
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 526
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 526
A;Patction:
A;Description: catalyzes the proteolytic activation of coagulation factor IX
A;Pathway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydrol
F;1-18/Domain: signal sequence #status predicted cSIG>
F;19-387/Product: coagulation factor XIa heavy chain #status experimental <HCH>
F;19-108/Domain: apple repeat <AP1>
F;19-108/Domain: apple repeat <AP2>
F;19-179/Domain: apple repeat <AP3>
F;388-625/Product: coagulation factor XIa light chain #status experimental <LCH>
F;388-625/Product: coagulation factor XIa light chain #status experimental <LCH>
F;388-618/Domain: trypsin homology <TRY>
F;20-103,514-581,571-599/Disulfide bonds: #status predicted
F;29/Disulfide bonds: interchain #status experimental
F;46-76,50-56,110-193,136-165,140-146,200-283,226-255,230-236,291-374,317-346,321-327,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 28-33;35-49,'X',51-55,'X',57-63;70-75,'X',77-79;107-109,'X',111-112;132-139;'
A;Residues: 28-33;35-49,'X',318-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375;
C;Comment: The proenzyme consists of two identical chains linked by one or more disulfide the active site, and a heavy chain, which associates with high molecular weight (HMW) kini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833 R;MCMullen, B.A.; Fujikawa, K.; Davie, E.W. Biochemistry 30, 2056-2060, 1991 Biochemistry 30, 2056-2060, 1991 A;Title: Location of the disulfide bonds in human coagulation factor XI: A;Reference number: A37940; MUID:91152017; PMID:1998667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 25, 2417-2424, 1986
A;Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tar
A;Reference number: A00920; MUID:86243360; PMID:3636155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P03951; GB:M18295
A;Note: the sequence shown follows the authors' translation
R;Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
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C;Date: 13-Aug-1986 #sequence revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A27431; A00920; A37940
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Blochemistry 26, 7221-7228, 1987
A;Title: Organization of the gene for human factor XI.
A;Reference number: A27431; MUID:88107663; PMID:2827746
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A; Residues: 1-625 < AS
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A; Residues: 1-625 < FUJ>
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C;Species: Canis Lupus
C;Date: 10-Sep-1999 #s
C;Accession: A30351; I
R;Evans, J.P.; Watzke,
                                                                                                                                                                                                                                                                  A,Cross-references: GB:M33826; NID:g163949; PIDN:AAA30844.1; PID:g163950 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; to C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-21/Domain: signal sequence #status predicted <SIG> F;22-40/Domain: propeptide #status predicted <SIG> F;22-40/Domain: Gla domain homology <GLA> C;Keywords: Gla domain domain homology <GLA> C;Keywords: Gla domain homology <GLA> C;Keywords: G;Keywords: G;Keyword
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A;Accession: I46201
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                                    F;41-452/Product: coagulation factor IX #status predicted F;90-121/Domain: EGF homology <EG1> F;127-163/Domain: EGF homology <EG2> F;127-163/Domain: EGF homology <EG2> F;218-445/Domain: trypsin homology <TRY> F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma F;46,47,54,55,59,60,65,66,69,72,73,738,134-148,150-163,171-F;57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-
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A;Title: Molecular cloning of a cDNA encoding canine
A;Reference number: A30351; MUID:89323338; PMID:27521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-452 < AXE>
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A; Residues: 1-452 < EVA>
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    ,306,402/Active site: His,
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Авр,
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                                         gamma-carboxyglutamic acid
3,171-326,243-259,373-387,39
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Query

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474.5;

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Length 452;

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F;142-180/Domain: E
F;184-293/Domain: C
F;300-361/Domain: C
F;366-430/Domain: C
F;445-679/Domain: t
                                                                                                                                                                                                                     A;Note: submitted:
A;Note: parts of tl
C;Genetics:
A;Gene: GDB:MASP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ra-reactive factor (EC 3.4.21.-) 2 precursor - human N;Alternate names: mannose binding protein-associated C;Species: Homo sapiens (man) C;Bate: 19-May-2000 #sequence_revision 19-May-2000 #te: C;Accession: A59271
                                                                                                                                                                                                                                                                                                                                                                                    A,Title: A second serine protease associated with mannan-binding lectin A;Reference number: A59271; MUID:97242412; PMID:9087411 A;Accession: A59271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
A59271
                                                                                                                                                                A;Cross-references: GDB:6071500
A;Map position: 1p36.2-1p36.3
C;Superfamily: complement-activ
                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:000187; GB:Y09926; A;Experimental source: tissue liver A;Note: submitted to GenBank, December 1996 A;Note: parts of this sequence, including the
                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Thiel, S.; Vorup-Jensen,
Nature 386, 506-510, 1997
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-686 < JE
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                                                                                                       ;Keywords: beta-hydroxyasparagine; complement pathway; duplication;
;1-15/Domain: signal sequence #status predicted <SIG>
;16-444,445-886/Product: Ra-reactive factor 2 #status predicted <MA
                                                                                          ;19-134/Domain: Clr/Cls repeat homology <ClR1>
                                                                                                                                                              Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homolo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VINOTTCENLLPQQITERMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDG
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C1r/C1s repeat homology <C1R2>
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4; Mismatches 172;
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homology
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trypsin (BC 3.4.21.4) precursor - Afric ;Species: Anopheles gambiae (African m C;Date: 13.7Jan-1995 #sequence_revision C;Accession: S40007 R;Mueller, H.
submitted to the EMBL Data
A;Reference number: S40003
A;Accession: S40007
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                          APGVQERRLKRIISH--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLCLSKGNPECDGKEDC-SDG----SDEKD---CD--CGLRSFTRQARVVGGTDADEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHT-----YRCLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQ---GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERSOFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP-----GQFTCRTGRCIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRPYPKLSSCTYSISLEEGFSVILDFVESFDVETHPET-LCPYDFLKIQTDREEHGPFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEK-----YCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLASPGFP-GEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAK---
                                                                                                                                                                                                                                                                                                                                                                             ALDIRMGTLKRLSPHYTQAWSEAVFIHEGYTHDAGFDNDIALIKLNNKVVINSNITPICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTLPHRIETKSNTVTITFVTDESGDHTGWKIHYTSTAHACPYPMAPPNGHVSPVQAKYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQVAPGEAPTCDHHCHNHLGGFYCSCRAGYVLHRNKRTCSALCSGQVFTQRSGELSSPEY
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(African mala
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                                           June
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                                                                                        malaria mosquito
n 13-Jan-1995 #te:
                                                                                                                                                                                                                                                                                                                                                                                                         --PFFNDFTFDYDIALLELEKPAEYSSMVRPICL
                                                                                                                    malaria mosquito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275;
                                                                                     #text_change 09-Jul-2004
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 RCDGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSC----
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 118 455 < SC2>
A; Residues: 118 455 < SC2>
C; Supperfamily: plasmin; kringle homology; plasminogen-related protein precur.
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine p
F; 1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental
F; 1-37.Domain: activation peptide (fragment) #status experimental <APT>
F; 34-117,118-252,264-455/Product: plasmin (fragments) #status experimental <
F; 37-114/Domain: kringle homology <KR4>
F; 118-455/Product: miniplasminogen #status experimental <MIN>
F; 126-205/Domain: kringle homology <KR5>
F; 226-455/Domain: kringle homology <KR5>
F; 226-448/Domain: trypsin homology <KRY>
F; 226-485/Domain: trypsin homology <KRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E. Protein Seq. Data Anal. 4, 69-74, 1991
A;Title: Complete amino acid sequence of equine miniplasminogen. A;Reference number: S17527; MUID:92052077; PMID:1946332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmin (EC 3.4.21.7) precursor - horse Wilternate names plasminogen N;Contains: miniplasminogen C;Species: Equus caballus (domestic horse)Date: 28-Oct-1994 #sequence revision C;Accession: A61545; S17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-275 <MUE>
A;Cross-references: UNIPROT:P35037; EMBL:Z22930;
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; procein digestion; serine
C;Keywords: hydrolase; procein digestion; serine
F;49-269/Domain: trypsin homology <TRY>
F;89,134,230/Active site: His, Asp, Ser #status p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-33;34-117 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Structural A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Schaller, J.; Rickli, Enzyme 40, 63-69, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: P80010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A61545
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Best Local Similarity
Matches 97; Conserv
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                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYKRGGKDACQGDSGGPL---VVDGKL--VGVVSWGFGCAMPGYPGVYARVAVVRNWVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQ--ITPRMMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIVGGFEIDVSETPYQVSLQYF-NSHRCGGSVLNSKWILTAAHCTVN-----LQPSSLA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQDEAVEDGTMTTVSGWGNTQSAAESNAILRAANIPTVNQKECTIAYSSSGGITDRMLCA
  Conservative
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Pred. No. 4.8e-24;
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353

Search Job ti	₽	8	Вb	ş	DЪ	ş	Вb	ş	Db	ş	망	ş	8	ş	Дb
Search completed: November 29, Job time : 30.3127 secs	438 YVRVSSFINWIE 449	667 YTRLPLFRDWIK 678	379 YLNGRVKSTELCAGI	607 LLPQQITPRMMCVG	320 AIITQNVIPACLPP	549 AEYSSMVRPICLPD	270ERSSRPSTYKV	489 DRGFRYSDPTQWTAI	221 KCSGR	429 DCDCGLRSFTRQARV	161 FTPEANPWANLEKN	401	102 PSVRWEFCNLRKC-	354 PAQTER-CSNGKCL	: : 57 KCQSWSSMTPH
), 2004, 08:33:22	19	78	YLNGRVKSTELCAGHLVGGVDSCQGDSGGPLVCFEKDKYILQ-GVTSWGLGCARPNKPGV	LLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGV	AIITQNVIPACLPPADYVVANWAECFVTGWGETQ-DSSNAGVLKEAQLFVIENKVCNRYE 378	ABYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCEN 606	ERSSRPSTYKVVLGTHHE-LRLAAGAQQIDVSKLFLEPSRADIALLKLSSP	DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP	KCSGRIVGGCVAIAHSWPWQISLRTRFGRHFCGGTLISPEWVLTAAHCL	AAHCYID	FTPEANPWANLEKNYCRNPDGDVNGPWCYTMNPQKLPDYCDVPQCESSPFDCGKPKVEPK	RCDCSDGSDE-K	PSVRWEFCNLRKC-SETVQEPSEPDCMLGIGKGYQGKKATTVTGTRCQAWAAQEPHRHSI	PAQTER-CSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTY	:
			437	666	378	606	319	548	269	488	220	428	160	400	101

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1: \cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: \cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: \cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

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16: \cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

16: \cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

18: \cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

19: \cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

10: \cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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Maximum Match 100%
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  GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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US-10-295-027-1185

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US-10-072-012-412

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US-10-072-012-420

US-10-072-012-420

US-10-072-012-420

US-10-072-012-42

US-10-072-012-44

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US-09-776-191-2

US-10-099-700A-2

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Sequence 1, Appli
Sequence 1185, Ap
Sequence 353, App
Sequence 412, App
Sequence 419, App
Sequence 419, App
Sequence 254, App
Sequence 120, App
Sequence 120, App
Sequence 1,2, App
Sequence 2, Appli
    4 US-10-267-219-2
4 US-10-1147-211A-2
5 US-10-127-21A-2
5 US-10-127-012-411
5 US-10-072-012-415
5 US-10-072-012-415
5 US-10-072-012-415
5 US-10-072-012-35
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5 US-10-072-012-414
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6 US-10-072-012-417
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6 US-09-978-193-169
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 Sequence 2, Appli
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Sequence 352, Appli
Sequence 411, App
Sequence 411, App
Sequence 1198, App
Sequence 1193, Ap
Sequence 2, Appli
Sequence 315, App
Sequence 315, App
Sequence 411, App
Sequence 411, App
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Sequence 110, Appli
Sequence 110, Appli
Sequence 110, Appli
Sequence 415, App
Sequence 415, App
Sequence 415, App
Sequence 416, Appli
Sequence 417, Appli
Sequence 418, Appli
Sequence 169, Appli
Sequence 169, App
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Sequence 1, Application US/10729807
Publication No. US20040132158A1

GENERAL INFORMATION:
APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer L.
APPLICANT: HANDMAN, Olga; HILLMAN, Jennifer L.
APPLICANT: TANG, Y. Tom; LAL, Preeti G.
APPLICANT: TYUE, Henry; AZIMZAI, YADIGA
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina N
TITLE OF INVENTION: HUMAN PEPTIDASES
FILE REFERENCE: PF-0651-1 DIV
CURRENT APPLICATION UNMBER: US/10/729,807
CURRENT FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US 09/889,238
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 60/172,247
PRIOR APPLICATION NUMBER: US 60/172,247
PRIOR APPLICATION NUMBER: US 60/172,247
PRIOR FILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: US 60/132,253
PRIOR TILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/136,653
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US-10-729-807-1
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL PROGRAM
SEQ ID NO 1
LENGTH: 762
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local S
Matches 679
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                                                                                                                                                                                              SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
                                                                                            LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                     FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                           FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                 SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
                                                                          LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
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Pred. No. 2e-275;
0; Mismatches
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US-10-166-709A-169
US-10-143-031A-169
US-10-143-030A-169
US-10-002-967A-169
US-10-017-083A-169
US-10-017-191A-169
US-10-143-029A-169
US-10-143-029A-169
US-10-143-029A-169
US-10-143-029A-169
US-10-145-017A-169
US-10-145-017A-169
US-10-164-728A-169
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CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
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publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compo
TITLE OF INVENTION: Methods of Screening for Modulators
FILE REFERENCE: 018501-012500US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                       R FILING DATE: 2001-12-14
R APPLICATION NUMBER: US 60
R FILING DATE: 2002-01-08
R APPLICATION NUMBER: US 60
R APPLICATION NUMBER: US 67
R FILING DATE: 2002-01-10
                                                                                                           FILING DATE: 2001-11-1.
APPLICATION NUMBER: US 6
APPLICATION NUMBER: US FILING DATE: 2002-02-1
                          APPLICATION NUMBER: US FILING DATE: 2002-02-08
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Glynne, Richard
Hevezi, Peter A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ginsberg, Wendy
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                              2002-02-08
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                                                                         60/347,349
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RESULT 3
US-10-072-012-353
US-10-072-012-353
Sequence 353, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1185
LENGTH: 855
TYPE: PRT
ORGANISM: Homo sapiens
S-10-295-027-1185
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Similarity 99.4%;
79; Conservative
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Pred. No. 2.2e-275;
0; Mismatches 4;
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APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Furtak, Katarzyna
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Entering APPLICATION NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: US/10/072,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Homo sapiens US-10-072-012-353
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PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR PPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/266,395
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
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Best Local Similarity
Matches 679; Conserv
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Andergon, David W.
Rastelli, Luca
Miller, Charles B.
Gerlach, Valerie
Taupier Jr, Raymond J
Gusev, Vladimir Y.
Colhan, Steven D.
Wolenc, Adam R.
Pena, Carol B. A
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                                    RSQFVVTSNSNKITVRFHSDQSYTDTGFLABYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                   SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
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              RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
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ilarity 99.4%;
Conservative
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; Pred. No. 2.2e:
0; Mismatches
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2.2e-275;
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APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Sample of Encoding 
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US-10-072-012-412
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Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond
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Grosse, William M.
Alsobrook II, John P.
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Padigaru, Muralidhara
Anderson, David W.
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Zerhusen, Bryan
Patturajan, Meera
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b. US20040033493A1
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Remaining Prior Application de
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 412
LENGTH: 855
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-412
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PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
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                                                                     QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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APPLICANT: BUTGESS, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Sam
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
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APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan Meera
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  LENGTH:
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R APPLICATION NUMBER: 60/265,395
DR FILING DATE: 2001-01-31
R APPLICATION NUMBER: 60/266,406
DR FILING DATE: 2001-02-02
R APPLICATION NUMBER: 60/266,767
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APPLICATION NUMBER: 60/267,057
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LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN 180
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                                                   FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
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Zerhusen, Meera
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
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Taupier Jr, Raymo
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5. US20040033493A1
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US-10-072-012-354 APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Enveries and Application of the Company of the C Sequence 354, Application US/ Publication No. US20040033493 GENERAL INFORMATION: APPLICANT: Tchernev, Velizar APPLICANT: Spytek, Kimberly APPLICANT:
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APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30 Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond Gusev, Vladimir Y. Colman, Steven D. Wolenc, Adam R. Pena, Carol E. A Shimkets, Richard Zerhusen, Bryan Patturajan, Mee Anderson, David W. Padigaru, Muralidhara Application US/10072012 o. US20040033493A1 Esha Luca

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; ORGANISM: Homo sapiens
US-10-072-012-354
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR APPLICATION NUMBER: 60/265, 395
PRIOR APPLICATION NUMBER: 60/266, 406
PRIOR APPLICATION NUMBER: 60/266, 406
PRIOR APPLICATION NUMBER: 60/266, 767
PRIOR APPLICATION NUMBER: 60/266, 767
PRIOR APPLICATION NUMBER: 60/267, 057
PRIOR APPLICATION NUMBER: 60/267, 057
PRIOR APPLICATION NUMBER: 60/266, 975
PRIOR APPLICATION NUMBER: 60/266, 975
PRIOR APPLICATION NUMBER: 60/267, 459
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 99.78; Conservative
                                                                                                                                                                                                                                                                                                                      SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                            ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                 ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                       SAAHCYIDDRGFRYSDPTQWTVFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                              SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAFGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                             C$D$SDEXDCDCGLR$FTRQARVV$GTDADEGEWPWQV$LHALGQGHICGA$LI$PNWLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPYYPGHYPPNIDCTWNIEVPNNQHVKVRPKFFYLLEPRRACGTCPKDYVEINGEKYCGE
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Pred. No. 4.5e-275;
0; Mismatches 5;
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US-10-072-012-420
US-10-072-012-420
; Sequence 420, Application US/10072012
making ation No. US20040033493A1
                                                                    ; TYPE: PRT
; ORGANISM: Homo
US-10-072-012-420
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Best Local
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SEQ ID NO 420
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/265,412
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                                                                                                                        LENGTH: 855
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                                                                                                                                                                                                                            APPLICATION NUMBER: 60/267,459
                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/266,975
                                                                                                                                                                                                                                                                           FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/266,767
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/266,406
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 678;
                   Similarity
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Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond (
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKPGVYTRLPLFRDWIKENTGV 855
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Grosse, William M.
Alsobrook II, John P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patturajan,
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 Conservative
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                99.1%;
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 Score 3756; DI
Pred. No. 4.5e
O; Mismatches
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DB 15;
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US-10-037-417-132

Sequence 132, Application US/10037417

Publication No. US20040052806A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P
APPLICANT: Tohernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A
APPLICANT: Betterajan, Meera
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Denise M
APPLICANT: Vernet, Corine A.M.
APPLICANT: John Burgess, Catherine E
APPLICANT: John Burgess, Catherine E
APPLICANT: John Burgess, Catherine E
APPLICANT: Li
APPLICANT: Li
APPLICANT: Li
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Rothenberg, Mark
APPLICANT: Rothenberg, Mark
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                                                   Edinger, Shlomit...
Edinger, Paul
Sciore, Paul
Bllerman, Karen
Malyankar, Uriel M
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Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
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CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR PILING DATE: 2001-01-05
PRIOR PILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-05
PRIOR PILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR APPLICATION NUMBER: 60/318,405
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 132
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 678;
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APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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APPLICATION NUMBER: 60/318,700
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    SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                  CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                           SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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                                                                                                                                                                                                           GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                            CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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99.3%;
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Pred. No. 4.5e-275;
0; Mismatches 5;
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APPLICANT: BUTGESS, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Enc.
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILLING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILLING DATE: 2001-01-31
PRIOR FILLING DATE: 2001-01-31
PRIOR FILLING DATE: 2001-01-31
PRIOR FILLING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILLING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,7459
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
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APPLICANT: Spytek, Ki
APPLICANT: Zerhusen,
APPLICANT: Patturajar
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APPLICANT:
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APPLICANT:
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Remaining Prior Application
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
150 ID NO 44
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Grosse, William M.
Alsobrook II, John P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Shimkets, Richard
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                                                                           data removed
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                                                                      File Wrapper or
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; Sequence 2, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES THEREON
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CURRENT APPLICATION NUMBER: US/09/776,191
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/213,124

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; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR PILING DATE: 2000-02-18
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FRSTSEQ for Windows Version 4.
; SEQ ID NO 2
; SEQ ID NO 2
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo Sapien
RESULT 11
US-10-099-700A-2
; Sequence 2, Application US/10099700A
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Pred. No. 6.4e-275;
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; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo 9
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Best Local Simi
Matches 678;
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GENERAL INFORMATION:
APPLICANT: Badyin L. Madison
APPLICANT: Edgar O. Ong
APPLICANT: Edgar O. Ong
ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE
TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: 24745-1613
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/10/099,700A
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/275,592
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 265
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                                                                   QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                                       ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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                  RNKPGVYTRLPLFRDWIKENTGV
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Pred. No. 6.4e-275;
0; Mismatches 5;
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Sequence 2, Application US/10190030B

Publication No. US20030134298A1

GENERAL INFORMATION:
APPLICANT: Madison, Edwin
APPLICANT: Ong, Edgar
TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASE 20,
TITLE OF INVENTION: METHODS BASED THEREON
FILE REFERENCE: 24745-1618
CURRENT APPLICATION NUMBER: US/10/190,030B
CURRENT FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 855
TYPE: PRT
ORGANISM: Homo Sapien
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                                                           QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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RNKPGVYTRLPLFRDWIKENTGV 855
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99.3%;
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Pred. No. 6.4e-275;
0; Mismatches 5;
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CURRENT APPLICATION NUMBER: US/10/302,840A; CURRENT FILING DATE: 2003-01-24; PRIOR APPLICATION NUMBER: 60/332,015; PRIOR APPLICATION NUMBER: 60/332,015; PRIOR FILING DATE: 2001-11-20; NUMBER: OF SEQ ID NOS: 18; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; SEQ ID NO 2; LENGTH: 855; TYPE: PRT; ORGANISM: Homo Sapien
US-10-302-840A-2
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US-10-902-840A-2
; Sequence 2, Application US/10302840A
; Publication No. US20030134794A1
; GENERAL INFORMATION:
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APPLICANT: Ong, Edgar O.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: POLYPEPTIDES AND METHODS BASED
FILE REFERENCE: 24745-1622
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                                                        QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                                 ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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          RNKPGVYTRLPLFRDWIKENTGV 683
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                                       QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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Pred. No. 6.4e-275;
0; Mismatches 5;
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; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo Sapien
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US-10-267-219-2
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APPLICANT: Yeh, Jiunn-Chern
APPLICANT: Yeh, Jiunn-Chern
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE
TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: 24745-1621
CURRENT APPLICATION NUMBER: US/10/267,219
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: 60/328,530
PRIOR APPLICATION NUMBER: 60/328,530
PRIOR FILING DATE: 09-0CT-2001
NUMBER OF SEQ ID NOS: 18
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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Best Local Similarity
Matches 678; Conserv
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 RNKPGVYTRLPLFRDWIKENTGV 683
                                                           QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ 660
                                                                                                                               ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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                                    QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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Pred. No. 6.4e-275;
0; Mismatches 5;
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PUBLICATION NO. US20030166851A1

GENERAL INFORMATION:
APPLICANT: Madison, Edwin
APPLICANT: Madison, Edwin
ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERI
ITILE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
ITILE OF INVENTION NUMBER: US/10/112,221A

CURRENT APPLICATION NUMBER: US/10/112,221A

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: 60/279,228

PRIOR APPLICATION NUMBER: 60/291,501

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

IENTIFICATION SECONDATE: 1001-05-15

NUMBER: FAST SECONDATE: 2001-05-15

NUMBER: FAST SECONDATE: 2001-05-15

NUMBER: FAST SECONDATE: 2001-05-15

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NUMBER: FAST SECONDATE: 2001-05-15
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US-10-112-221A-2
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                                                         ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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Pred. No. 6.4e-275;
0; Mismatches 5;
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Sequence 2, Application US/10104271

| Publication No. US20030181658A1
| GENERAL INFORMATION: GEWIN
| APPLICANT: Madison, Edwin
| APPLICANT: Madison, Edwin
| APPLICANT: Jiunn-Chern Yeh
| TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE CVSP14, THE
| TITLE OF INVENTION: POLYPEPTIDES AND METHODS BASED THEREON
| FILE REFERENCE: 24745-1614
| CURRENT APPLICATION NUMBER: US/10/104,271
| CURRENT FILING DATE: 2002-03-20
| PRIOR APPLICATION NUMBER: 60/278,166
| PRIOR APPLICATION NUMBER: 60/278,166
| PRIOR APPLICATION NUMBER: 60/278,166
| PRIOR FILING DATE: 2001-03-22
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
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; ORGANISM: Homo
US-10-104-271-2
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                                                                                           SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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                                                                                                                                            CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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Pred. No. 6.4e-275;
0; Mismatches 5;
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Publication No. US20030235900A1
GENERAL INFORMATION:
APPLICANT: Madison, Edward
APPLICANT: Yeh, Jiunn-Chern
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 1(
TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: 24745-1616
CURRENT APPLICATION NUMBER: US/10/147,211A
CURRENT APPLICATION NUMBER: US/10/147,211A
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/291,001
PRIOR FILING DATE: 2001-05-14
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 855
TYPE: PRT
CORGANISM: Homo Sapien
US-10-147-211A-2
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US-10-147-211A-2
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                                                        SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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Pred. No. 6.4e-275;
0; Mismatches 5;
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US-10-156-214A-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local Similarity
Matches 678; Conserv
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APPLICANT: Joseph Edward Semple
APPLICANT: George P. Vlasuk
APPLICANT: Scott Jeffrey Kemp
APPLICANT: Mallareddy Komandla
APPLICANT: Daniel Vanna Siev
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CURRENT APPLICATION NUMBER: US/10/156,214A
CURRENT FILING DATE: 2002-05-23
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ORGANISM: Homo Sapien
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                                                               CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV 480
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                                       CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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Pred. No. 6.4e-275;
O; Mismatches 5;
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                                                                                                                        APPLICANT: Lapley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR APPLICATION NUMBER: 60/266,975
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US-10-072-012-352
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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 352
LENGTH: 855
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                                                                                              PRIOR APPLICATION NUMBER: 60/267,459 PRIOR FILING DATE: 2001-02-08
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Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
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Spytek, Kimberly
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Gerlach, Valerie
Taupier Jr, Raymond J.
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Anderson, David W.
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Shimkets, Richard
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Sequence 411, Application US/100;
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Syytek, Kimberly
APPLICANT: Serhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muralidha:
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
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Local Similarity 99.3%;
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, Muralidhara
, David W.
, Luca
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Pred. No. 6.4e-275;
0; Mismatches 5;
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APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A.
APPLICANT: Lepley, Denise M.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Enc.
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: 60/265, 512
FRIOR APPLICATION NUMBER: 60/265, 512
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 514
PRIOR APPLICATION NUMBER: 60/265, 514
PRIOR APPLICATION NUMBER: 60/265, 517
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR APPLICATION NUMBER: 60/266, 406
PRIOR FILING DATE: 2001-01-31
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Best Local S
Matches 678
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 411
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TYPE: PRT
ORGANISM: Homo :
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                                                                                                                        RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
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                        GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                  RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
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Pred. No. 6.4e-275;
0; Mismatches 5;
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APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Enc
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,406
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-05
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US-10-072-012-418
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APPLICATION NUMBER: 60/266,767
FILING DATE: 2001-02-05
APPLICATION NUMBER: 60/267,057
FILING DATE: 2001-02-07
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Taupier Jr, Raymond
Gusev, Vladimir Y.
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Grosse, William M.
Alsobrook II, John P.
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Padigaru, Muralidhara
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PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 418
FENOTE: 655
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-418
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Best Local (
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              RNKPGVYTRLPLFRDWIKENTGV
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RNKPGVYTRLPLFRDWIKENTGV
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855
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RESULT 22
US-10-600-187-2
J. Sequence 2, Application US/10600187
Publication No. US20040086910A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi

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TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/10/600,187
CURRENT FILING DATE: 2003-06-20
FRIOR APPLICATION NUMBER: US/9/654,600A
FRIOR FILING DATE: 2000-09-01
FRIOR FILING DATE: 2000-09-01
FRIOR APPLICATION NUMBER: 09/421,213
09/027,337
FRIOR FILING DATE: 1999-10-20
1998-02-20
INUMBER OF SEQ ID NOS: 98
SEQ ID NO 2
LENGTH: 855
TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
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OTHER INFORMATION: TADG-15
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             RNKPGVYTRLPLFRDWIKENTGV
                                                ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWYTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                   SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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RNKPGVYTRLPLFRDWIKENTGV 855
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Conservative
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99.3%;
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Pred. No. 6.4e-275;
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GENERAL INCOMP.

APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SOFTWARE: CUSTOM
FIGHER OF SEQ ID NOS: 2700
GRANISM: Homo sapiens
US-10-276-774-1798
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Publication No. US20040053245A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                       SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                            CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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                      QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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                                                      ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQY
                                                                                                       SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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Pred. No. 3e-274;
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PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1143
LENGTH: 851
TYPE: PRT
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APPLICANT: HYBEG INC
TITLE OF INVENTION: NO. US20040053248A1e1
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11.18
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  RNKPGVYTRLPLFRDWIKENTGV 683
                                                                  QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRIFQAGVVSWGDGCAQ
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                                         QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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Pred. No. 3e-274;
1; Mismatches 6;
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CURRENT EILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILLING DATE: 2001-03-14
PRIOR FILLING DATE: 2001-03-14
PRIOR FILLING DATE: 2001-03-25,149
PRIOR FILLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/274,967
PRIOR FILLING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 782
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Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Manjula GANNAVARAPU
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Best Local S
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
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hes 604; Conserv
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                                                                  SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
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Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                         SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
                                                                                                                           LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
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Karen GLATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karen LU
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APPLICANT: Allen, Keith D
APPLICANT: Allen, Michael W.
APPLICANT: Leviten, Michael W.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING SEITITLE OF INVENTION: PROTEASE GENE DISRUPTIONS
FILE REFERENCE: R-386
CURRENT APPLICATION NUMBER: US 60/217,449
PRIOR APPLICATION NUMBER: US 60/217,449
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-900-751-2
                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 855
TYPE: PRT
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Matches
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                                                                                                                                                                                                                Query Match
Best Local :
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                 LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                               FPNSPYPAHARCQWVLRGDADSVLSLTFRSFDVAPCDEHGSDLVTVYDSLSPMEPHAVVR
                                                                                FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
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83.2%;
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Pred. No. 9.7e-234;
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          APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-258
FULR REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr., Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
                                                                                                                                                             Pena, Carol E. A
Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
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Gangolli, Esha
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; ORGANISM: Mus musculus
US-10-072-012-355
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 355
LENGTH: 855
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Best Local Similarity 83.2%;
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R APPLICATION NUMBER: 60/265,395

DR FILING DATE: 2001-01-31

DR APPLICATION NUMBER: 60/266,406

DR FILING DATE: 2001-02-02

DR APPLICATION NUMBER: 60/266,767

DR APPLICATION NUMBER: 60/266,767
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FILING DATE: 2001-02-07
APPLICATION NUMBER: 60/266,975
FILING DATE: 2001-02-07
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APPLICATION NUMBER: 60/265,517
FILING DATE: 2001-01-31
APPLICATION NUMBER: 60/265,412
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              QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ 660
                                                                              ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                       SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAFGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                            SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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QTTCEDLMPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSAEKDGRMFQAGVVSWGEGCAQ
                                                                                                                                                                                 CSDGSDEKNCDCGLRSFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLV
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                                                                                                                      SAAHCFQDDKNFKYSDYTMWTAFLGLLDQSKRSASGVQELKLKRIITHPSFNDFTFDYDI
                                                            ALLELEKSVEYSTVVRP1CLPDATHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVIN
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; Pred. No. 9.7e-234;
59; Mismatches 56;
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; Remaining Prior Application d; NUMBER OF SEQ ID NOS: 1391 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 413 ; SEQ ID NO 413 ; LENGTH: 855 ; TYPE: PRT ; ORGANISM: Mus musculus US-10-072-012-413
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
FILE CATHERING: 21402-258
CURRENT APPLICATION: Proteins and Nucleic Acids Enc.
FILE REFERENCE: 21402-258
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-05
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US-10-072-012-413
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Matches 568; Conserv
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FILING DATE: 2001-02-07
APPLICATION NUMBER: 60/266,975
FILING DATE: 2001-02-07
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Grosse, William M.
Alsobrook II, John P.
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Taupier Jr, Raymond
Gusev, Vladimir Y.
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Spytek, Kimberly
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o. US20040033493A1
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; Pred. No. 9.7e-234;
59; Mismatches 56;
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APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Bryan
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Gangolli, Esha
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
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     APPLICANT:
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                                                                                                                    Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKPGVYTRLPLFRDWIKENTGV 683
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                                Pena, Carol E. A
Furtak, Katarzyna
Grosse, William M.
                                                                   Colman, Steven D. Wolenc, Adam R. Pena, Carol E. A
                                                                                                                                                                                                                                                                     Patturajan, Meera
Shimkets, Richard
   Alsobrook II,
Lepley, Denis
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5. US20040033493A1
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Muralidhara
                                                                                                                                                                                                       David W
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APPLICANT: Burgess, Catherine E.
FILE REFERENCE: 21402-258
CURRENT APPLICATION: PROTEINS and Nucleic Aci
FILE REFERENCE: 21402-258
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
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PRIOR APPLICATION NUMBER: 60/266,412
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PRIOR APPLICATION NUMBER: 60/266,406
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 356
LENGTH: 855
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ORGANISM: Rattus
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SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAFGVQERRLKRIISHFFFNDFTFDYDI
                                                                                                                    GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                   CSDGSDEKNCDCGLRSFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLV
                                                                     CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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83.0%; Pred. No. 7.8e-233;
tive 59; Mismatches 57;
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APPLICANT: BUTGESS, Catherine E.
FITLUE OF INVENTION: Proteins and Nucleic Acids Enc
FITLE REPERENCE: 21402-258
CURRENT APPLICATION UNMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR PPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR PPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
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PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-07
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PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-31
PRIOR FILLING DATE: 2001-01-31
PRIOR FILLING DATE: 2001-01-31
PRIOR PELLOATION NUMBER: 60/265,517
PRIOR PELLOATION NUMBER: 60/265,412
PRIOR PELLOATION NUMBER: 60/265,412
PRIOR PELLOATION NUMBER: 60/265,395
PRIOR PELLOATION NUMBER: 60/266,406
PRIOR PELLOATION NUMBER: 60/266,406
PRIOR PELLOATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR PILLING DATE: 2001-02-05
PRIOR PILLING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILLING DATE: 2001-02-08
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PRIOR FILLING DATE: 2001-02-08
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APPLICANT: Spytek, Kimberly
APPLICANT: Sprtek, Kimberly
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
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                                               Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 414
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LENGTH: 855
TYPE: PRT
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Pena, Carol E. A
Furtak, Katarzyna
Grosse, William M.
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Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Rieger, Daniel K.
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Anderson, David W.
Rastelli, Luca
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Shimkets, Richard
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Patturajan, Meera
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5. US20040033493A1
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Best Local Similarity
Matches 567; Conserv
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                                                                                                                                                             SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                                                                                         RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQGFTCRTGRCIRKELRCD
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                                              QTTCEELLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEKDGRIFQAGVVSWGEGCAQ
                                                              QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                             SAAHCFQDETIFKYSDHTMWTAFLGLLDQSKRSASGVQEHKLKRIITHPSFNDFTFDYDI
                                                                                                                                                                                              CSDGSDEKNCDCGLRSFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLV
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                                                                                                                                                                                                                                           SIGKCLPQSQQCNGKDDCGDGSDEASCDNVNAVSCTKYTYRCQNGLCLNKGNPECDGKKD
                                                                                                                                                                                                                                                            SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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                                                                                                                                                                                                                                                                                                                    GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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Search completed: November 29, 2004, 08:49:50 Job time : 94.8166 secs

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3: //cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
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825, Appl
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RESULT 1 US-09-027-337-2

ALIGNMENTS

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Sequence 2, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
LENGTH: 855
TYPE: PRT
ORGANISM: Homo sapiens
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                                                        ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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 QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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                                  ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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Patent No. 6451500

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: Overexpressed in Carcinomas

FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/644,600

CURRENT APPLICATION NUMBER: 09/421,213

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: 09/471,337

PRIOR FILING DATE: 1998-02-20
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SEQ ID NO 2
LENGTH: 855
TYPE: PRT
ORGANISM: Homo sapiens
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                LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN 180
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Pred. No. 3.9e-262;
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Score 3754; DB 2; Pred. No. 3.9e-262; 0; Mismatches 5;

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Query Match

OTHER INFORMATION: Amino acid sequence of TADG-15
OTHER INFORMATION: 23 to 2589 of Sequence 1
Patent No. 5972616
3-09-027-337-2

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APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: O'verexpressed in Carcinomas

FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CURRENT FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 09/421,213

09/027,337

PRIOR FILING DATE: 1999-10-20

1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 2

LENGTH: 855
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US-09-654-600A-2
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Patent No. 6649741
GENERAL INFORMATION:
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                     CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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APPLICANT: Tanimoto, Hicotoshi
FITLE OF INVENTION: TADG-15: An Extracellular Serine Pro
FITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
I PRIOR FILING DATE: 1999-02-7,337
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 10
LENCTH: 902
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OTHER INFORMATION: Epithin
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                             FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ 120
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SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                    GWADCPDYSDERYCRONATHOFTCKNOFCKPLFWVCDSVNDCGDGSDEEGCSCPAGSFKC
                                                                      GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                      RSQFVVSSNSSKITVHFHSDHSYTDTGFLAEYLSYDSNDPCPGMFMCKTGRCIRKELRCD
                                                                                                                                         RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                                                                                                                       SPYYPGHYPPNINCTWNIKVPNNRNVKVRFKLFYLVDPNVPVGSCTKDYVBINGEKGSGE
                                                                                                                                                                                                       SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYYEINGEKYCGE
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82.9%;
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Indels

Gaps

0

360 472 412 240 352 292

232 60

902; 0

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Sequence 10, Application US/09654600A

Patent No. 6649741

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: O'verexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/654,600A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
INUMBER OF SEQ ID NOS: 98
SEQ ID NO 10
LENGTH: 902
TYPE: PRT
ORGANISM: Mus musculus
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US-09-654-600A-10
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OTHER INFORMATION: Epithin
09-654-600A-10
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                                           RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                    FPNSPYPAHARCQWVLRGDADSVLSLTFRSFDVAPCDEHGSDLVTVYDSLSPMEPHAVVR
                                                                                                                                                                                                                    FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
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 GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                             LCGTFSPSYNLTFLSSQNVFLVTLITNTGRRHLGFEATFFQLPKMSSCGGVLSDTQGTFS
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APPLICANT: Semple, Joseph Edward
APPLICANT: Coombs, Gary Samuel
APPLICANT: Reiner, John Eugene
APPLICANT: Ong, Edgar O.
APPLICANT: Ong, Edgar O.
APPLICANT: Araldi, Gian Luca
TITLE OF INVENTION: Inhibitors of Serine Prote
TITLE OF INVENTION: MTSP1
FILE REFERENCE: Corvas 255/049
CURRENT APPLICATION NUMBER: US/09/657,986B
CURRENT EILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 241
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-657-986B-2
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                                                                                   ASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRWMCVGFL
                                                                                                                                             FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPD
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                             SGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENTG
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CCLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEFAX: (617) 876-5851
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08200900A Patent No. 5665566
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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STREET: 87 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP 218
                                                                             429
                                                                                                                                                                                                                                                                                                                                                                                         219 RRACGTCPKDYVBI-NGEKYCGERSQFV------VTSNSNKITVRFHSDQSYTDT 266
484 HCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALL 543
                                      QCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAA 603
                                                                                                                                                                                                                                 DAGH--QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNG 374
                                                                                                                                                                                                                                                                         GFKANFTTGYGLGIPEPCKEDNFQCKDGECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTT 464
                                                                                                                                                                                                                                                                                                                                                                                                                               ELP--TDCGGPHDLWEPNTTFTSINFPNSYPNQAFCIWNLNAQKGKNIQLHFQEFDLEN-
                                                                           DCD---CGLRSFTRQA--RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAA 483
                                                                                                                                                        KDDCGDGSDEASC-----PKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 428
                                                                                                                                                                                              DSSGLVQFRIQS----IWHV----ACAEN--
                                                                                                                                                                                                                                                                                                                                                  -----IADVVEIRDGE---GDDSLFLAVYTGPGPVNDVFSTTNRMTVLFITDNMLAKQ 404
                                                                                                               ---LGTGNSSVPTFSTGGGPYVNLNTAP-----NGSLILTPSQQC-----LEDSLILL 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     798 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%; Score 703.5; DB 1; 32.6%; Pred. No. 1.5e-42;
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                                                                                                                                                                                              -----WITQISDDVC-----QLLG 499
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                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application Patent No. 6746859
                                                                                                                                                                                        Matches 181;
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GITELECOMMUNICATION INFORMATION
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                      161 QLPRMSSCGG--RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEP 218
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GFLAEYLS---YDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSDELNC-----SC 316
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                                                     ----IADVVEIRDGE---GDDSLFLAVYTGPGPVNDVFSTTNRMTVLFITDNMLAKQ 404
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87 CambridgePark Drive
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Matches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                     Query Match
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TOPOLOGY: line
MOLECULE TYPE: |
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/0061
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                                                                                                                                                                                                                                                  Local Similarity
wes 181; Conserv
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                                                                   GFLAEYLS---YDSSDPC-PGQFTCRTGRCIRKELRCDGWADCTDHSDELNC----SC
                                                                                                        ----IADVVEIRDGE---GDDSLFLAVYTGPGPVNDVFSTTNRMTVLFITDNMLAKQ 404
                                                                                                                                      RRACGTCPKDYVEI-NGEKYCGERSQFV------VTSNSNKITVRFHSDQSYTDT 266
                                                                                                                                                                              ELP--TDCGGPHDLWEPNTTFTSINFPNSYPNOAFCIWNLNAQKGKNIQLHFQEFDLEN-
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DAGH--QFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNG
                                    GFKANFTTGYGLGIPEPCKEDNFQCKDGECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTT
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US-09-734-675-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09734675
Patent No. 6365391
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 407
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WEBSTER, Marion et al TITLE OF INVENTION: ISOLATED HUMAN PROTEASE TITLE OF INVENTION: NUCLEIC ACID MOLECULES TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CL000862
                                                                       665
                                    389
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                                                                                                                                                                                                               AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLL
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                                      GVYTRVTALRDWITSKTGI 407
                                                                                                                                      PQ----QITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKP
                                                                                                                                                                                                                                                  ----TYKNPARWTASFGV-----TIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSP
                                                                                                                                                                                                                                                                                     DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
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                                                                  GVYTRLPLFRDWIKENTGV 683
                                                                                                          POAYNDAITPRMLCAGSLEGKTDACOGDSGGPLVSSDARDIWYLAGIVSWGDECAKPNKP
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                                                                                                                                                                                                                                                                                                                                                                                                          15.5%; Score 588; DB 3; 45.9%; Pred. No. 1.4e-34;
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ENCODING HUMAN
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RESULT 12
US-09-879-792-14
; Sequence 14, Application US/09879792
; Patent No. 6734006
; GENERAL INFORMATION:
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US-09-685-166A-895
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 895
TENCTH: 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.8%; Score 560.5; DB 4; Best Local Similarity 33.9%; Pred. No. 1.7e-32; Matches 131; Conservative 58; Mismatches 128;
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ORGANISM: Homo sapiens
-09-685-166A-895
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APPLICANT:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
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                                                                                                                                           TŚWGSGCAKAYRPGVYGNVMVFTDWI 484
                                                                                                                                                                                                                                                                                                                                                                                   PEWIVTAAHCVEKP----LINNPWHWTAFAGILRQSFMFYGAGYQ---VQKVISHPNYDSK
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Carter, Darrick
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Kalos, Michael D.
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RESULT 13 US-09-679-426-895

Sequence 895, Application US/09679426 Patent No. 6759515

GENERAL

INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Xu, Jiangchun Dillon, Davin C. Mitcham, Jennifer L.

Harlocker, S Jiang, Yuqui

Susan L. ui Robert A.

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

APPLICANT:

APPLICANT:

Henderson, Robert Kalos, Michael D. Fanger, Gary R. Stelter, Marc W. Stelk, John A. Day, Craig H. Vedvick, Thomas (

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; ORGANISM: Homo
US-09-879-792-14
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PRIOR FILLING DATE: 2000-06-13
PRIOR PELLORTION NUMBER: US 60/283,353
PRIOR FILLING DATE: 2001-04-13
PRIOR PELLORTION NUMBER: US 60/283,648
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR FILLING DATE: 2001-04-16
PRIOR FILLING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local :
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APPLICANT: Gedrich, Richard
TITLE OF INVENTION: Regulation of Human Transmembrane
TITLE OF INVENTION: Protease
FILE REFERENCE: 02973.00035
CURRENT APPLICATION NUMBER: US/09/879,792
CURRENT FILING DATE: 2001-06-13
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                                   VSWGDGCAQRNKPGVYTRLPLFRDWI 677
                                                                                             EIRVINOTTCEN--LLPQQITPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRI-FQAGV
                                                                                                                                                                                TFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKG
                                                                                                                                                                                                                                                                                               ACSSKAVVSLRCLACGVNLNS-SROSRIVGGESALPGAWPWQVSLH-VQNVHVCGGSIIT
                                                                                                                                                                                                                                                                                                                     GSDEK-----DCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLIS 475
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TSWGSGCAKAYRPGVYGNVMVFTDWI
                                                                       KVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGPL--VTSNNNIWWLIGD
                                                                                                                                                 TKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEEKGKTSEVLNAA 400
                                                                                                                                                                                                                       PEWIVTAAHCVEKP----LINNPWHWTAFAGILROSFMFYGAGYO---VOKVISHPNYDSK
                                                                                                                                                                                                                                                              PNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS-QRSAPGVQERRLKRIISHPFFNDF
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APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, DAvid H.-F.
APPLICANT: Teng, DAvid H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TMPRSS2 is a Tumor Suppr FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/342,749
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-749-2
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US-09-342-749-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-895
                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09342749
Patent No. 6166194
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REFERENCE: 210121.427020
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
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; SOPTWARE: PatentIn Ver. 2

; SEQ ID NO 2

; LENGTH: 492

; TYPE: PRT

ORGANISM: Homo sapiens
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/691,840
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US/09/342,749
PRIOR APPLICATION NUMBER: US/09/342,749
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US-09-691-840-2
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Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/091,044
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                             Local Similarity
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GSDEK-----DCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLIS
                                                                                                                        GSKCSNSGIECDSSGTCINPSNWCDGVSHCPGGEDENRCVRLYGPNFILQVYSSQRKSWH 169
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33.9%; Pred
37;
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Pred. No. 2.3e-32;
57; Mismatches 129
                                                                                                                                                                                                                             DB 4;
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RESULT 16
US-08-944-483-65
; Sequence 65, Ap
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                                    US-08-944-483-65
 Query Match
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                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acid
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: STROUPE,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
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                                                                      TOPOLOGY: lir
                                                                                                       TYPE: amino acids
                                                                                                                                                                                              TELEFAX:
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CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
STROUPE, NOVEL SERINE PROTEASE REAGENTS
VENTION: NO METHODS USEFUL FOR DETECTING AND TREATING DISEASES
VENTION: OF THE PROSTATE
SEQUENCES: 76
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US-08-807-151-3
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                                                     Query Match 14.4%;
Best Local Similarity 43.5%;
Matches 103; Conservative 50
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APPLICANT: Bandman, Ol
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: Filed Hes
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
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LIBRARY: GenBa
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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CITY: Palo Alto
STATE: CA
                                                                                                                                           CLONE:
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ZIP: 94304
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                                                                                                                                                                                                                                TYPE: amino acid
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443 VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDFTQWTA 502
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IBM Compatible
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                                                     Score 544.5; DB
Pred. No. 1e-31;
50; Mismatches
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US-09-478-957-3
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Best Local S
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INFORMATION FOR SEQ ID NO: 3:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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MEDIUM TYPE: Diskette
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APPLICANT: Lal, Preeti
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                    TYPE: amino a STRANDEDNESS:
                                                                                                                                             Local Similarity
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CLASSIFICATION:
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CITY: Palo Alto
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TELEFAX: 415-845-4166
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OPERATING SYSTEM:
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                                                                                                                               103;
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   VLGLHMASNLTSPQIETRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPE
                                                                IVGGSDSREGAWPWVVALYFDDQ-QVCGASLVSRDWLVSAAHCVYG----RNMEPSKWKA
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US-10-177-661-4
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Sequence 4, Application
Patent No. 6794173
GENERAL INFORMATION:
APPLICANT: Anderson, Di
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RESULT 19
US-09-518-046-2
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CURRENT APPLICATION NUMBER: US/09/518,046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261,416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 2
SEQ ID NO 2
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APPLICANT: Underwood, Lowell J.

TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof

TITLE OF INVENTION: IN Ovarian Carcinoma and Uses Thereof
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OTHER INFORMATION: complete amino acid
OTHER INFORMATION: protein
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                                                                                368
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                                                                                                          TTC--ENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQ-AGVVSWGDGC
                                                                                                                                                                                             LLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQ
                                                                                                                                                                                                                                           AAHCVYD-----LYLPKSWTIQVGLVSLLDNPAP---SHLVEKIVYHSKYKPKRLGNDIA
                                                                                                                                                                                                                                                                                                                      GHVVTLQCTACGHRR-GYSSRIVGGNMSLLSQWPWQASLQFQGY-HLCGGSVITPLWIIT
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                                      AQRNKPGVYTRLPLFRDWIKE 679
                                                                                                                                                                                                                                                                                    AAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIA
                                                                                                                                                                                                                                                                                                                                                                GS-DEKDCD-CGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRCRSSFKCIELITRCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWKTMCSDDWKGH 137
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AEVNKPGVYTRVTSFLDWIHE
                                                                              KICHHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPL--VCQERRLWKLVGATSFGIGC
                                                                                                                                                               LMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISN
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Pred. No. 2.5e-31;
446
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08681151 Patent No. 5869637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE FILE REFERENCE: 3256-4 CURRENT APPLICATION NUMBER: US/10/177,661 CURRENT FILING DATE: 2002-06-20 PRIOR APPLICATION NUMBER: US 60/299,606 PRIOR PELING DATE: 2001-06-20 NUMBER OF SEQ ID NOS: 6 NOS: 6 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Au-Your
APPLICANT: Bandman
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ORGANISM: Homo sapiens
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat.
COMPUTER: DO
COM
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A NOVEL HUMAN KALLIKREIN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                           STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                          COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 DYLVYDSYLTPRMMCAGDLRGGRDSCQGDSGGPL-VCEQNNRWYLAGVTSWGTGCGQRNK
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Bandman, Olga
Braxton, Scott Michael
Goli, Surya
                                                                                          IBM Compatible SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                             INCYTE PHARMACEUTICALS,
                                                                                                                                                  Diskette
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TELEPHONE: 415-855-0555
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PRIOR APPLICATION DATA:
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CLONE: 205011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNNIHCOFFTYATKAFHRPEYRKSCLLKRSSSGTPTSIKPVDNLVSGFSLKSCALSEIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATFFQLPRMSSCG---GRIRKAQGTFNSPYYPGHYPP-----NIDCTWNIE-----V 200
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                               RDYVITKOMICAGYKEGGIDACKGDSGGPL-VCKHSGRWOLVGITSWGEGCARKEQPGVY
                                                                                       PQQ-ITPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRIFQAGVVSWGDGCAQRNKPGVY
                                                                                                                                               LNYTEFOKPICLPSKADTNTIYTNCWVTGWGYTKERGETONILOKATIPLVPNEECOKKY
                                                                                                                                                                                                                                                                         GIPY--PDVWRIYGGILNLSEITNKTP---FSSIKELIIHQKYKMSEGSYDIALIKLQTP
                                                                                                                                                                                                                                                                                                                                 GFRYSDPTQWTAFLGLHDQSQ--RSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- OFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSGRPSPPIIQENAVSGYSLFTCRKARPEPCHFKI----YSGVAFEGEELNATFVQGAD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSD-PCP------GQFTCRTGR---CIRKELRCDGWADCTDHSDELNCSCDAGH-
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Pred. No. 6.3e-30;
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; LOCATION: (1)..(418)
; OTHER INFORMATION: Xaa = unknown
US-10-177-661-6
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                                                                                                                                                     RESULT 23
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Sequence 2, Application US/10177661
Patent No. 6794173
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Virca, G. Duke
TITLE OF INVENTION: DENDRITIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.5.
7 129; Conservative
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APPLICANT: Virca, G. Duke
TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE
FILE REFERENCE: 3256-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/177,661
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 60/299,606
PRIOR FILING DATE: 2001-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
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OTHER INFORMATION: Consensus sequence
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                                                                                                                                                                                                                      345
                                                                                                                                                                                                                                                                                                      285 XPGTTCWIXGWGATXEXXGKTSPVLQEAXVPLIDNKXCNSYXVYDNXITPRMICAGYLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                    514 APGVQERRLKRIISHPFFNDFTF-----DYDIALLELEKPAEYSSMVRPICLPDASHVF 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 CKPLFWVCDSVNDCGDNSDEQGC----SCPAQTFRCSNGKCLSK---SQQCNGKDDCGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 NWNESYSXXACXQMGXXSAXYXSEXGXXXRXGANSFXKLNVSPXNLLXXDXYTSXIQXXL 121
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                                                                                                                                                                                                                                                            GVDSCQGDSGGPL---SSVEADGRIFQAGVVSWGDGC-AQRNKPGVYTRLPLFRDWI 677
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      TRANSMEMBRANE SERINE
      PROTEASE
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; FILE REFERENCE: 3256-A
; CURRENT APPLICATION NUMBER: US/10/177,661
; CURRENT FILING DATE: 2002-06-20
pRIOR APPLICATION NUMBER: US 60/299,606
pRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
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                      623 SGGVDSCQGDSGGFLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWI 677
                                                                               351
                                                                                                                  566 VFPAGKAIWVTGWGHT-QYGGTGALILQKGEIRVINQTTCENLL--PQQITPRWMCVGFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 CPKHAVRCDGVVDCKLKSDELGCVRFDWDKSLLKIYSGSSHQ------WLPICS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 CIRKELRCDGWADCTDHSDELNC-----SCDAGHQFTCKNKFCKPLFW--VCD
                                                                                                                                                                                             LHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASH
                                                                                                                                                                                                                                      WPWQVSLH-FGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEG-----WKVYAGTSN
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RGGRDSCQGDSGGPL-VCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWI
                                                                            TFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDL
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                                                                                                                                                            LHQLPEAAS-----IAEIIINSNYTDEEDDYDIALMRLSKPLTLSAHIHPACLPMHGQ
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US-09-879-792-12
US-09-879-792-12
Sequence 12, Application US/09879792
Patent No. 6734006
GENERAL INFORMATION:
APPLICANT: Kido. Yonghong
APPLICANT: ALOR Yonghong
ITILE OF INVENTION: Regulation of Human Transmembrane Serine
TITLE OF INVENTION: Protease
FILE REFERENCE: 02973.00035
CURRENT APPLICATION NUMBER: US/09/879,792
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/283,353
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: PCT
PRIOR PRIOR APPLICATION NUMBER: PCT
PRIOR APPLICATIO
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283; 23;

Gaps

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176 579 118

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RESULT 25
US-08-807-151-1
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Best Local Similarity 32.5
Matches 135; Conservative
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APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
TITLE OF INVENTION: PROTEASE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/807
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3174 Porter Drive
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                                                                      415-845-4166
                                                                                                                                                                                                                                                                                                                                                                         FastSEQ Version 2.0
                                                                                      415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals,
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                                                                                                                                                                                                                                                                                                                              US/08/807,151
                                                                                                                                   PF-0227
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Best Local Similarity
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      TELEPAX: 415-040-1:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SERRICH: 283 amino acids
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TOPOLOGY:
IMMEDIATE SOURCE:
LIBRARY: SCORNOTO1
TONE: 556016
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APPLICANT: Bandman
APPLICANT: Lal, P
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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ADDRESSEE: Incyte Pl
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TITLE OF INVENTION: NOVEL HU
TITLE OF INVENTION: PROTEASE
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                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
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                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 --VTSKNNIWWLIGDTSWGSGCAKAYRPGVYGNVMVFTDWI 275
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                                                                                                             415-855-0555
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                                                                                                                                                                                                                                                                   08/807,151
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                                                                                                                                                        PF-0227
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RESULT 27
US-08-508-448C-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5804410
GENERAL INFORMATION:
APPLICANT: Kazuyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08508448C Patent No. 5804410
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                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: sir
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KAZUYOSHI YAMAOKA et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Com
OPERATING SYSTEM:
SOFTWARE: Wordper
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FILING DATE: July 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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CLONE: 556016
   STRANDEDNESS:
                     TYPE:
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                                                                                                                                                                                                                                              FILING DATE:
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                                    LENGTH: 418 amino acids
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CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82, Appli
Patent No. 6444425
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo E
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APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roaddh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US
FILE REFERENCE: 210121.475C1
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APPLICANT: Reed, Steven G.
APPLICANT: Medes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT APPLICATION NUMBER: US 09/285,323
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
SEQ ID NO 83
APPLICANT: LOGGE, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: THE THERAPY AND METHODS FOR
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 418
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; TYPE: PRT
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US-09-370-838-83
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                                                                                                                                                                                                                                                                                                                Sequence 82, Application Patent No. 6759508 GENERAL INFORMATION:
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; ORGANISM: Homo sapien US-09-854-133-82
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L--VQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWIRQQTGI 418
                                                                              QEYAGHTVPELRQGQVRIISNDVCN--APHSYNGAILSGMLCAGVPQGGVDACQGDSGGP
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ADI65326

ADI748695

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches 679
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                                                                                                                                                                                          GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                           RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
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                                                                                                                          SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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                                        CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                  GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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27-MAY-1999;
                       This sequence represents a human peptidase, designated HPEP-1. The invention relates to 18 human peptidases designated HPEP-1 to HPEP-18, respectively. The peptidases can be used for treating a disease or condition associated with decreased expression or over expression of functional human peptidases. The diseases that can be diagnosed, prevented and treated include cell proliferative disorders (such as arteriosclerosis, psoriasis, myelofibrosis, and cancers), autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies, Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple sclerosis, and scleroderma), infections, and metabolic disorders (such addition's disease, diabetes, cystic fibrosis, glycogen storage disease
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Yue H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated polypeptide for diagnosis, prevention and proliferative, autoimmune/ inflammatory and metabolic
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Best Local S
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                         Matriptase, serine protesse; human; breast cancer; pre-maligna calumic keratosis; leukoplakia; Barett's epithelium; columnar metaplasis; ulcerative colitis; bowenoid papulosis; adenomatous colorectal polyp; Qyerat erythroplasia; vulvar intraepithelial neoplasia; tumour; metastasis; therapy
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CC The zymogen (inactive) form of matriptase is a single-chain protein. The CC active 2-chain form strongly interacts with fragments of a Kunitz-type CC serine protease inhibitor (hepatocyte growth factor activator inhibitor, CC HA1-1) to form SDS-stable complexed form. Dreast cancer cells, matriptase CC in detected in human milk. The invention is directed to a method of Cd detecting a malignancy or a pre-malignant lesion in breast or other CC tissue by detecting the presence of single- or 2-chain forms of CC matriptase in the tissue. The object is to inhibit tumour onset, tumour CC growth and metastasis. Malignancies and pre-malignant conditions CC characterised by expression of the zymogen or activated form of CC matriptase are treated by administering an inhibitor of matriptase, CC especially a Bowman-Birk inhibitor. The pre-malignant condition is CC elekoplakia, Barrett's epithelium of the esophagus, ulcerative colitis, CC disease, bowenoid papulosis, vulvar intraepithelial neoplasia or CC dysplatic changes to the cervix. The invention also provides methods for in vivo or in vitro diagnosis of malignancy or pre-malignant lesion, and CC inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the full-length form of human matriptase, a trypsin-like protease. This has an additional 172 amino acids compared with the truncated form of matriptase given in AAB19551. Either form can be produced in transformed or transfected cells using a claimed method. The
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Region
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Best Local S
Matches 679
                                                                                                                                                                                                                  Human membrane-type serine protease MT-SP1.
02-OCT-2000; 2000WO-US027250
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Pred. No. 4.7e-241;
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Query Match
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RNKPGVYTRLPLFRDWIKENTGV
                                                                                                                                                                                                                                                                                                                                                                                           CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWFWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
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                                                                                                                       QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                                                                                                                                    ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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                                                                                                                                                                         ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                   SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                                                                                               CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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99.4%;
                                                                   TPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRIFQAGVVSWGDGCAQ
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Pred. No. 4.7e-241;
0; Mismatches 4;
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26-FEB 2001
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14-MAR-2001
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29-MAR-2001
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29-MAR-2001
29-MAR-2001
30-MAY-2001
11-APR-2001
11-APPR-2001
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08-FEB-2001;
09-FEB-2001;
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05-FEB-2001;
07-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; cardiomyopathy; atheroselerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI16817;
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    2001US-0272788

2001US-02759369

2001US-02759369

2001US-02759899

2001US-02758999

2001US-02764489

2001US-02764599

2001US-0276769

2001US-0276769

2001US-02787789

2001US-02787789

2001US-02787789

2001US-02787789

2001US-02801479

2001US-02830439

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2001US-0271664P.
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2001US-0271855P.
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2001US-0266767P.
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thereof, which have properties related to the stimulation of biochemical corphysiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of converse pathological conditions. The present invention describes novel than and murine NOVX proteins, as well as methods to modulate their cexpression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX associated disorders, e.g. cardiomyopathy, catherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune cdiscorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, carthritis, Alzheimer's disease, infections, stroke, muscular dystrophy condeplepsy. Accordingly, these molecules have many activities including cytostatic, cardiant, antidiabetic, antiarteroisclerosic, anorectic, antiarteroisclerosics.
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Best Local
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07-SEP-2001;
07-SEP-2001;
12-SEP-2001;
19-SEP-2001;
18-OCT-2001;
18-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiasthmatic, nephrotropic, antiarteriosclerotic, anorectic, neuroprotective, nootropic, antiatratricic, hepatotropic, neuroprotective, nootropic, antiatratricic, hepatotropic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.
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Gerlach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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Gangolli EA, Pad
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Sangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller
VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE
K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burges
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                                                                                                                                                LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                                                                   FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                                                                                                                                                                                                                                                     MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
                                                                                                                                                                                                                                    FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                                                                                                                                                                                                                    MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
         SPYYPGHYPPNIDCT
                                                      SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVBINGEKYCGE
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2001US-0318115P.

; 2001US-0318740P.

; 2001US-0323379P.

; 2001US-0330308P.

; 2001US-0332701P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.
                                                                                                                     YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3760; DB 5;
Pred. No. 4.7e-241;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
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biochemical
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RESULT 6

RESULT 6

RAD116883
ID AD1116883
ID AD116883
ID AD16883
ID AD17 15-J
AC AD11
XX AD17
AC AD11
XX AD17
AC AD17
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                        31-JAN-2001;
02-FEB-2001;
05-FEB-2001;
07-FEB-2001;
07-FEB-2001;
08-FEB-2001;
09-FEB-2001;
15-FEB-2001;
26-FEB-2001;
27-FEB-2001;
27-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                 31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
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Human NOVX protein homologue SeqID 419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                                                                                                                                                                                                                                                   RNKPGVYTRLPLFRDWIKENTGV 855
                                                                                                                                                                                                                                                                                                                                                      RNKPGVYTRLPLFRDWIKENTGV 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLELEKPAEYSSMVRPICLPDASHVPPAGKAIMVTGMGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                          QTTCENLLPQQ1TPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGR1FQAGVVSWGDGCAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                          (first entry)
                                                                                                                                                                       protein;
                                                                                                                                                                         855
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human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.

2002WO-US002785.

2001US-0265517P.
2001US-0266406P.
2001US-0266767P.
2001US-0266975P.
2001US-0267823P.
2001US-0267823P.
2001US-0267823P.
2001US-0271864P.
2001US-0271835P.
2001US-0271855P.
2001US-0272788P. 2001US-0265395P. 2001US-0265412P. 2001US-0265514P.

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This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical cor physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel thuman and murine NOVX proteins, as well as methods to modulate their CC man and murine NOVX proteins, as well as methods to modulate their CC resting or preventing NOVX-associated dispress and antibodies are useful in CC treating or preventing NOVX-associated dispress, e. cardiomyopathy, CC atheroscierosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC treating or preventing diseases such as inflammation, autoimmune CC disorders, altergies, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, and artificially the company of the contractivity in the conditions, stroke, muscular dystrophy and conditions.
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15-MAR 2001

16-MAR-2001

16-MAR-2001

20-MAR-2001

26-MAR-2001

26-MAR-2001

29-MAR-2001

29-MAR-2001

11-APR-2001

11-AP
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Gerlach
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14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX
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19-SEP-2001;
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epilepsy. Accordingly, these moleculostatic, cardiant, antiinflammatory,
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Gangolli EA, Pad
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Gangolli EA, Padigaru M, Anderson DM, I
VL, Taupier RJ, Gusev VY, Colman SD,
K, Grosse WM, Alsobrook JP, Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides and nucleic acids, useful for preventing on NOVX-associated disorders, e.g. cancer, cardiomyopathy, lerosis, or diabetes, and in chromosome mapping, tissue
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2001US-0276397P
2001US-0278652P
2001US-0278778P
2001US-0279884P
2001US-0279884P
2001US-0283992P
2001US-0283279
2001US-028327P
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2001US-028327P
2001US-028327P
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2001US-0294747P
2001US-0294747P
2001US-03128474P
2001US-03128474P
2001US-03128474P
2001US-0315477P
2001US-031874PP
2001US-03130308P
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2001US-0275925P.
2001US-0275947P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 419; 1498pp; English
                      these molecules
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                      have many activities
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Rastelli L, Mill
, Wolenc AR, Pena
M, Rieger DK, Buj
                   muscular dystrophy
v activities including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue typing
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Pena CEA;
Burgess
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RESULT 7
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ID ADD11
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AC ADD1
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DT 15-A
XX

ADI16876; ADI16876

standard;

protein;

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15-APR-2004

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiasthmatic, nephrotropic, antiarthritic, hepatotropic, neuroprotective, nootropic, antibacterial, virucide, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmacogenomics. of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                           661
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                RNKPGVYTRLPLFRDWIKENTGV
                                                                                                                                 ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                            SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                          SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                   GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                            RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAEERVVMLPPRARSLKSFVVTSVVAFFTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
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RNKPGVYTRLPLFRDWIKENTGV
                                                       SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                 GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                          RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
                                                                                    QTTCENLLPQQ1TPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGR1FQAGVVSWGDGCAQ
                                                                                                                ALLELEKPAEY
                                                                                                                                                                        SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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                                                                                                                  SSMVRPICLPDASHVFPAGKAIWVTGWGHTQ
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Pred. No. 4.7e-241;
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                            683
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Human

XVON

protein

homologue

SeqID 412

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14. MAR - 2001
114. MAR - 2001
115. MAR - 2001
116. MAR - 2001
116. MAR - 2001
116. MAR - 2001
120. MAR - 2001
220. MAR - 2001
230. MAR - 2001
111. APR - 2001
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119. APR - 2001
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31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
02-FEB-2001;
07-FEB-2001;
07-FEB-2001;
08-FEB-2001;
08-FEB-2001;
15-FEB-2001;
15-FEB-2001;
27-FEB-2001;
21-MAR-2001;
14-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabe inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200268649-A2
                                     2001US-0265395P
2001US-0265511PP
2001US-0265511PP
2001US-0266767PP
2001US-0266767PP
2001US-02677057PP
2001US-0267459PP
2001US-0271839PP
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2001US-02776450PP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephropathy; cirrhosis; arthritis;
infection; str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; diabetes;
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Tchernev VT, Spytek KA, Zerhusen BL Li L, Gangolli EA, Padigaru M, And Gerlach VL, Taupier RJ, Gusev VY, Furtak K, Grosse WM, Alsobrook JP, Zerhusen BD, Anderson DW, R
VY, Colman SD,
UP, Lepley DM, Patturajan M, Rastelli L, Wolenc AR, , Rieger DK, Rastelli Shimkets RA; Pena CEA; Miller CE; Burgess CE;

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

Disclosure; SEQ ID NO 412; 1498pp; English.

CC or physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel CC human and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polynucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, catherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy CC and epilepsy. Accordingly, these molecules have many activities including CC cytostatic, anti-HTV, antidiabetic, antiarteriosclerotic, anorectic, correspondentive, nootropic, antibacterial, virucide, antiparasitic, crelaxant and anticonvulsant. In addition, they are useful in screening CC assays to identify small molecules that modulate or inhibit, for example, correspondentic, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and coff the invention. This invention thereof, which lor physiologica. invention. relates to have proper properties a novel related to the stimulation of polypeptides biochemical

Sequence 855 AA;

망 5 S 밁 Ś S S 밁 밁 멼 밁 5 Query Match Best Local : Matches 361 473 301 413 241 353 181 293 233 173 121 61 679; ب Similarity SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVBINGEKYCGE LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN Conservative 99.2%; 0, Score Pred. Mismatches 3760; DB 5; No. 4.7e-241; Length Indels 855; 0; Gaps 420 472 300 412 240 352 180 292 120 232

CURAGEN

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ADN39A
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AX ADN3
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AX CAND
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XX III-II
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AN ADN3
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21-NOV-2001
29-NOV-2001
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13-FEB-2002
20-FEB-2002
20-FEB-2002
20-FEB-2002
20-APR-2002
11-JUN-2002
15-JUN-2002
                           Afar D,
Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibrotic disorder; psoriasis; ischaemia; heart disease; atheroscleros inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; disgnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN39867
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ic disorder; psoriasis; ischaemia; heart disease; athe
                           Aziz N,
Murray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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                                                                                                                                        2001US-035066P.
2001US-033439AP.
2001US-033439AP.
2001US-034731AP.
2002US-034721AP.
2002US-034734P.
2002US-035671AP.
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2002US-037873AP.
2002US-039783AP.
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2002US-0397845P.
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                                                                                                BIOTECHNOLOGY INC
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                           Ginsburg WM,
R, Watson SR,
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                           Gish KC,
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Determining the presence or absence of a pathological cell in a useful for diagnosing, prognosing or treating cancer, comprises a nucleic acid in a biological sample.
                                                                                                                                                                                                                    WPI; 2003-468649/44.
N-PSDB; ADN39650.
                                                                                                                                                   The invention relates to nucleic acids and proteins
                                                                                                                                                                   Claim 12; SEQ
                                                                                                                                                                  ID NO C237; 1385pp; English.
                                                                                                                                                                                            patient,
detecting
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cc whose expression is upregulated or downregulated in specific cancers or cother diseases such as angiogenic or fibrotic disorders, and to methods co fetermining the presence or absence of a pathological cell in a cc patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The current in also relates to expression vectors and host cells comprising a curleic acid of the invention; antibodies which specifically bind a cc polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the collipse and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal conevascularistation syndromes, scarring and uterine fibroids. They may calso be useful in wound healing and in contraception. The present (ADN38683-ADN40064)

Sequence 855 AA;

Matches 679; Query Match Best Local

Similarity

99.2**%**; 99.4**%**;

Score 3760; DB 7; Pred. No. 4.7e-241; Mismatches

Length Indels

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ALLELEKPAEYSSMVRPICLPDASHVPPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                       ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                            SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQSRRLKRIISHPFFNDFTFDYDI
                                                                                                               CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                   SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                  GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                  GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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Matches 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bodary
Wu TD;
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                                                                                                                                                    LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                                                                                                                   MABERVVMLPPRARSLKS FVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
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                                                                                                                         LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                      FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
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                              SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
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Pred. No. 4.7e-241;
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15-FEB-2001;

26-FEB-2001;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabe inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma;
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5 밁 ঠ В S 밁 S

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This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel human and murine NOVX protectins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polymucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy CC and epilepsy. Accordingly, these molecules have many activities including C cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
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Gerlach
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golli EA, Padigaru M, Anderson DW, Rastel
, Taupier RJ, Gusev VY, Colman SD, Woler
Grosse WM, Alsobrook JP, Lepley DM, Rieg
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M, Rieger DK, Burges
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(first entry)

Human NOVX protein homologue SeqID 354

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Gangolli EA, ch VL, Taupie c K, Grosse W Taupier ¥, RJ, Guecc , Alsobrook JP, RJ, Gusev VY, Anderson DW, Y, Colman SD, Lepley Ņ, Rastelli Wolenc A Rieger , g, r Z, Miller CE Pena CEA; Burgess Œ; ä

New NOVX polypeptides and nucl treating NOVX-associated diso atherosclerosis, or diabetes, d nucleic acids, useful for preventing or disorders, e.g. cancer, cardiomyopathy, etes, and in chromosome mapping, tissue typing or

Disclosure; SEQ ID NO 354; 1498pp; English

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome athmospheric acthma immunodeficiency syndrome athmas acthma athmas at mass at a such as athmas at a such as athmas at a such as athmas at a such as a such as athmas at a such as athmas at a such at a such as a such a (AIDS) obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, arthritis, Alzhelmer's disease, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic, antiarthritic, hepatotropic, anorectic, antiasthmatic, nephrotropic, antiarthritic, hepatotropic, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and farmacogenomics. This polypeptide is a homologue of a human NOVX protein

1 MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDFCPGQFTCRTGRCIRKELRCD SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDS FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG ${ t RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD}$ SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN Conservative 99.1%; 0; Score 3756; D Pred. No. 8.6e 0; Mismatches 3756; No. 8 .6e-241; les 5; DB 5 VNDCGDNSDEQGCSCPAQTFRC Length 855; Indels SKGNPECDGKED <u>.</u>. Gaps 420 532 360 472 300 240 352 180 292 120 232

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Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA; Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE; Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA; Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess C Pena CEA; Burgess CE;

2002-706998/76. DB; ADI16507.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing pharmacogenomics. or

Claim 1; SEQ ID NO 44; 1498pp; English

This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes movel thuman and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polymuclectides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, and epilepsy. Accordingly, these molecules have many activities including CC vctostatic, cardiant, antinflammatory, immunosuppressive, antiallergic, antiasthmatic, nephrotropic, antiarteriosclerotic, anorectic, constraints, cardiant, antinflammatory, immunosuppressive, antiallergic, nephrotropic, antiarteriosclerotic, antiarterioc antiasthmatic, nephrotropic, antiarteriosclerotic, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening creations, they are useful in screening answer to identify small molecules that modulate or inhibit, for example,

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              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75
                                                   antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                             standard;
                                                                                                                                                                                                       RNKPGVYTRLPLFRDWIKENTGV 683
                                                                                                                                                                                                                                                             QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                                                                                                                                                                                                                            ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                                                                                                                                                                                                               SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                                                                                                                                                 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAEERVVMLPPRARSLXSFVVTSVVAFPTDSXTVQRTQDNSCSFGLHARGVELMRFTTPG 60
                                                                                                                                                                                             RNKPGVYTRLPLFRDWIKENTGV
                                                                                                                                                                                                                                                                                                                                              SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                                                                                                                                CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPYYPGHYPPNIDCTWNIEVPNNQHVKVSFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                                                                                                                                            QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                                                                                                                                                                                                             ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
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                                                                           (first
              ovary
                       derived gene-15; TADG-15; serine protease;
                                                   derived gene-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                             protein;
                                                                           entry
              cancer;
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Pred. No. 1e-240;
0; Mismatches 5;
             carcinoma; diagnosis
                                                   (TADG-15)
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                                                                                                                                                                                           757
                                                   protein.
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WPI; 1999-527418/44.
N-PSDB; AAX87815.
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                                                                                                                                              20-FEB-1998;
                                                                                                                                                         18-FEB-1999;
                                                                                                                                                                               WO9942120-A1
                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                  (UYAR-) UNIV
                                                                                          new extracellular serine protease
                                                                                                                                                                                                                                                                                                                                        sapiens
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                                                                               10;
                                                                                                                       Tanimoto
                                                                                                                                  ARKANSAS
                                                                                                                                              98US-00027337
                                                                                                                                                         99WO-US003436
                                                                                                                                                                                                 614. .615
615. .855
                                                                                                                                                                                                                                                                                                 109.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                           note=
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                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                 note= "cytoplasmic
                                                                                                                                                                                           note=
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                                                                                                                                                                                                                                                        note= "ligand-binding repeat
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                                                                               English.
                                                                                                                                                                                           "catalytic domain"
                                                                                                                                                                                                                       "conserved
                                                                                                                                                                                                                                  "conserved SDE motif"
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                                                                                                                                                                                                                                                                                           "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                "CUB repeat"
                                                                                                                                                                                                                                                                    is N-glycosylated'
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                                                                                           for
                                                                                                                                                                                                                                                                                                                  domain"
                                                                                          diagnosis
                                                                                                                                                                                                                                                          (class
                                                                                           of neoplastic disease
                                                                                                                                                                                                                                                         A motif) "
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The present sequence represents a novel human extracellular serine protease, termed tumour antigen derived gene-15 protein (see AAY06671), that is overrexpressed in breast and ovarian carcinomas. The TADG-15 gene (see AAX87815) can be used as a diagnostic and therapeutic target in ovarian carcinoma and other carcinomas including breast, prostate, lung and colon. The ligand binding domains of TADG-15 may be valuable in the uptake of specific molecules into tumour cells. The invention also provides: a vector that is capable of expressing DNA encoding TADG-15 protein; host cells selected from bacterial cells (especially Escherichia coli), mammalian cells, plant cells and insect cells; and a method of detecting expression of TADG-15 protein using a hybridisation probe Sequence 855 AA;

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Matches
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                                                                                                           Local Similarity
mes 678; Conserv
  233
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                                                                      1 MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
                  FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                       MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
    FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                            Conservative
                                                                                                                       99.1%;
                                                                                                           0.
                                                                                                           Score 3754; DB 2;
Pred. No. 1.2e-240;
0; Mismatches 5;
                                                                                                                                    Length 855;
                                                                                                            Indels
                                                                                                           0,
                                                                                                            Gaps
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121

LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN

Gaps

292

232

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RESULT 14
AAB98500
ID AAB98
XX AAB98
XX AAB98
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Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                 20-OCT-1999;
                                                                                                                                                                                                                                                       20-OCT-2000;
                                                                                                                                                                                                                                                                                             26-APR-2001
                                                                                                                                                                                                                                                                                                                                 WO200129056-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TADG-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB98500 standard; protein;
                                                                              2001-381031/40.
DB; AAH23601.
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      16-OCT-2001
                                          AAE06930;
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                                                                                                                                                                              RNKPGVYTRLPLFRDWIKENTGV
                                                                                                                                                                                                     RNKPGVYTRLPLFRDWIKENTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPYYEGHYEDNIDCTWNIEVENNQHVKVRFKFFYLLEERRACGTCFKDYVEINGEKYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
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                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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nilarity 99.3%;
Conservative
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      (first entry)
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                                                                              protein;
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Pred. No. 1.2e-240;
0; Mismatches 5;
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18-FEB-2000;
22-JUN-2000;
26-JUL-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                         The invention relates to transmembrane serine proteases and their corresponding nucleotides and the protease domain of a type-II membrane-type serine protease (MTSP). MTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in gene therapy. The present sequence is human MTSP1 protein (also called matriptase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel single chain polypeptide comprising protease domain of type-II membrane-type serine protease or its catalytically active portion useful for treating and preventing cancer and tumor.
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                                                                                                                                                                                                                                                                    Sequence
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SPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
                                                                     LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
                                                                                                                FPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTVYNTLSPMEPHALVQ
                                                                                                                                                   MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
                                           LCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN
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; 2000US-0213124P.
; 2000US-0220970P.
; 2000US-00657986.
; 2000US-0234840P.
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                        Score 3754; DB 4; Pred. No. 1.2e-240; "" amatches 5;
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ease; tumour; cancer; cytostatic;
                                                                                                                                                                                                                                        Length
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                                                                                              New transmembrane serine protease 7 (MTSP7) polypeptide for diagnosing neoplastic diseases, monitoring tumor progress or therapeutic effectiveness, or identifying MTSP7 modulators for treating tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; type-II membrane-type serine protease neoplastic disease; pre-malignant lesion; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA022929
                                                                                                                                                                                                       N-PSDB; AAL53444.
                                                                                                                                                                                                                                 WPI; 2002-732827/79.
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Disclosure;

Page 172-174; 184pp; English

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RESULT 17
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Best Local S
Matches 678
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                                                                                                                                                                                                      QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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                                                                                                                                                                             QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
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Pred. No. 1.2e-240;
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Human NOVX protein homologue
                                     15-APR-2004
                                                                                                        ADI16816 standard; protein; 855
                                     (first entry)
   SegID 352
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human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str. Homo sapiens.

31-JAN-2001
02-FEB-2001
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11-MAR 31-JAN-2002; WO200268649-A2 2001US-0279882P.
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2001US-028014Fy.
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2001US-0283083P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polynucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (Ig) an ephropathy, cirrhosis, carchinitis, Alzheimer's disease, infections, stroke, muscular dystrophy CC and epilepsy. Accordingly, these molecules have many activities including CC vcostatic, cardiant, antinflammatory, immunosuppressive, antialregic, CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, CC neuroprotective, noortopic, antibacterial, virucide, antiparasitic, celasars and anticonvulsant. In addition, they are useful in screening CC assays to identify small molecules that modulate or inhibit, for example, CC used as in chromosome mapping, tissue typing, preventive medicine and CC used as in chromosome mapping, tissue typing, preventive medicine and CC of the invention.
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Best Local S
Matches 678
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Gerlach
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Gangolli BA, Padigaru M, Anders
Ch VL, Taupier RJ, Gusev VY, Col
K, Grosse WM, Alsobrook JP, Le
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JP, Lepley DM,
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Rastelli L, Miller CE;
Wolenc AR, Pena CEA;
N, Rieger DK, Burgess C
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14-MAR-2001;
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Alzheimer's disease; infection; str.
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This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism. CC specifically, it refers to the use of biologically active fragments for cidagnostic and prognostic assays and furthermore in the treatment of CC disgnostic and prognostic assays and furthermore in the treatment of CC chuman and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polynucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, cratdiant, antinflammatory, immunosuppressive, antiallergic, antiastentic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, cantiasthmatic, natinflammatory, immunosuppressive, antiallergic, antialergic, an
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Gangolli EA, Pad
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Taupier RJ, Gusev VY, Colman SD,
rosse WM, Alsobrook JP, Lepley DM,
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RNKPGVYTRLPLFRDWIKENTGV
                                                                                                              ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                                   SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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                                                                                                                                                    SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma;
                                                         Human NOVX
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                                                                                                                                            protein;
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or

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09-FEB-2001
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31-JAN-2001;
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Alzheimer's disease; infection; str.
                 ev VT, Spytek KA, Zerhusen E
Gangolli EA, Padigaru M, Ar
h VL, Taupier RJ, Gusev VY,
K, Grosse WM, Alsobrook JP,
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2001US-0265511PP.
2001US-0265511PP.
2001US-0266767PP.
2001US-0266767PP.
2001US-02677057PP.
2001US-0267759PP.
2001US-0267859PP.
2001US-02771839PP.
2001US-02775947PP.
2001US-02775947PP.
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2001US-0278652PP.
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2001US-028832PP.
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               Anderson DW, I
VY, Colman SD,
UP, Lepley DM,
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                                                                       Patturajan M,
                                  jan M, Shimkets RA;
Rastelli L, Miller
Wolenc AR, Pena C
                 Rieger DK,
                                    Pena CEA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cd diagnostic and prognostic assays and furthermore in the treatment of cdiverse pathological conditions. The present invention describes novel chuman and murine NOVX proteins, as well as methods to modulate their cc expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polymucleotides and antibodies are useful in cc treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, cc atherosclarosis, cancer and diabetes. Furthermore, they may be used in ctreating or preventing diseases such as inflammation, autoimmune cd disorders, allergies, blood disorders, acquired immunodeficiency syndrome cd disorders, allergies, blood disorders, acquired immunodeficiency syndrome cd disorders, allergies, blood disorders, acquired immunodeficiency syndrome cd disorders, allergies, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, chaemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, constructive, nootropic, antisathericic, hepatotropic, cantiallergic, relaxant and anticonvulsant. In addition, they are useful in screening cassays to identify small molecules that modulate or inhibit, for example, consideration, wound healing and anglogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and coff the invention.
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Matches 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel nucleic acids, and encoded pol thereof, which have properties related to the stimulation of bic or physiological responses in a cell, tissue, organism. Specifically, it refers to the use of biologically active fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                   CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                        SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                    GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                                       SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                 GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDS
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CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
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Pred. No. 1.2e-240;
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                                                                                                                                                   VNDCGDNSDEQGCSCPAQTFRC
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biochemical
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The present invention describes a polypeptide comprising a purified single or two chain polypeptide, which comprises the protease domain of a type-II membrane-type serine protease (MTSP10) or its catalytically cative portion, or a mutein of it, where up to 50 % of the amino acids are replaced with another amino acid, and the resulting polypeptide is a single chain or two chain polypeptide that has a catalytic acitivity of at least 1-10 % of the unmutated polypeptide. WTSP10 has cytostatic cativity. The polypeptide containing the protease domain of the WTSP10 is useful for detecting a neoplastic disease, and for diagnosing the presence of a pre-malignant lesion, a madignancy, or other pathologic condition in a subject, or monitoring tunour (e.g. breast, cervix, prostate, lung, ovary or colon tumour) progression and/or therapeutic effectiveness. An inhibitor of the polypeptide containing the protease comain of MTSP10 is useful for treating or preventing meoplastic disease in a mammal. An inhibitor of the activation cleavage of the zymogen form of the WTSP10 polypeptide is useful for inhibiting tumour initiation, carvit in the e.g.
                                                                                                                                                                                                                                                                                                                                                               New polypeptides comprising the protease domain of a type-II membrane-
type serine protease (MTCP10), or its muteins, useful for diagnosing
neoplasms or malignancies, or for screening for MTCP10 inhibitors for
treating such diseases.
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DB; ABZ22450.
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Best Local
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                 RNKPGVYTRLPLFRDWIKENTGV
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RNKPGVYTRLPLFRDWIKENTGV
                                                 QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                                                QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGFLSSVEADGRIFQAGVVSWGDGCAQ
                                                                                                      ALLELEKPAEYSSMVRPICLPDASHVPPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                     ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                         SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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Serine protease 17; CVSP17; tumour; cancer; antisense therapy; prostate; breast; cervix; lung; ovary; colon; gene therapy; human; enzyme; MTSP1; protease;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New substantially purified serine protease 17 polypeptide and encoding nucleic acid, useful for diagnosing and treating tumor conditions and/cancer, particularly of the breast, cervix, prostate, lung, ovary or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 175-177; 189pp; English.
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               CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                        SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                     GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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                                                 The invention relates to type II membrane-type serine protease 9 (MTSP9) polypeptides and polynucleotides. MTSP belongs to type II transmembrane serine protease (TTSP) family. Sequences of the invention and their antibodies are useful for diagnosing, treating or preventing neoplastic disease in mammals. They are useful for monitoring tumour progression, inhibiting tumour initiation, growth or progression or treating malignant or pre-malignant conditions. Transgenic animals of the invention are useful in animal models of tumour initiation, growth and/or progression models. The invention is also useful in gene therapy. The present sequence is human membrane-type serine protease 1 (MTSP1). MTSP1 also referred as matriptase is a member of the TTSP family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New substantially purified single or two-chain type II membrane-type serine protease 9 (MTSP9) polypeptide, useful for monitoring tumor progression, inhibiting tumor initiation, or treating a malignant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; type II membrane-type serine protease 9; tumour; transgenic; type II transmembrane serine protease; enzyme; gene therapy; WTSP9; neoplastic disease; transgenic animal; membrane-type serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 183-185; 199pp; English
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15-MAY-2001; 2001US-0291501P.
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Query Match Best Local Similarity

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Matches 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 855 AA;
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N-PSDB; AAD47180.
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                                                               ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                         SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                          CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                                                                      SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
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  QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ
                                       ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                     SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane serine protease 1 (MTSP1). The invention relates to novel human type II transmembrane serine protein 20 (MTSP20) (see ABP72374) and nucleic acids encoding it (see ABE58499). Also claimed are methods of inhibiting tumour initiation, growth or progression by inhibiting MTSP20 activity, and of treating or preventing a disease or disorder associated with undesired and/or uncontrolled angiogenesis or neovascularisation, especially undesired angiogenesis associated with solid neoplasms, vascular malformations and cardiovascular disorders, chronic inflammatory diseases, aberrant wound repairs, circulatory disorders, crest syndromes, dermatological disorders and ocular disorders using an inhibitor of MSP20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New type-II membrane-type serine protease 20 polypeptides, useful for preparing a medicament for diagnosing, treating or preventing cancer, dermatological disorders, aberrant wound repairs or crest syndromes.
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cytostatic; dermatological; cardiant; vulnerary; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 198-200; 216pp; English.
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      New purified single- or
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The invention relates to human type I transmembrane serine protease 25 (MTSP25; ADB97565) and polypeptides derived from it (e.g., ADB97555). The CR (MTSP25 gene is located on chromosome 12. MTSP25 is a serine protease comprising an A chain and a B chain linked by a disulphide bond. MTSP25 is expressed or is active in tumour cells, and can therefore be used as a clasmostic marker for certain cancers. The invention also encompasses complete acids encoding an MTSP25 polypeptide (ADB9754, ADB9757), and clastic acids encoding an MTSP25 polypeptide (ADB97564, ADB9757), and clastic acids encoding an and host cells comprising an MTSP25 polypucleotide; a MTSP25 knockout animal; and an antibody specific for ceither the single chain (zymogen) or two-chain (activated) form of MTSP25. MTSP25 polypeptides are useful in diagnosing, preventing or treating neoplastic diseases, such as cancer of the breast, cervix, prostate, lung, ovary or colon. MTSP25 polypeptides may also be used for identifying compounds that modulate the protease activity of the color and for monitoring tumour progression and/or therapeutic effectiveness. The present sequence represents the related protein, MTSP1 (also known as matriptase).
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                                                                                                                                                                                                  The invention comprises a conjugate that consists of a therapeutic agent and a peptide substrate (optionally linked via linker). The peptide substrate is proteolytically cleaved by a cell surface protease prasoluble, released or shed form of it, to liberate the therapeutic agent, the conjugate of the invention is not substrantially cleaved by plasmin or protease specific antigen (PSA). The conjugate of the invention is useful for treating a cell-surface protease-associated disease such as: cancer, ocular diseases, cardiovascular diseases, chronic inflammatory diseases, wounds, circulatory disorders, dermatological disorders, rheumatoid arthritis, psoriasis, diabetic retinopathies, recurrence of pterygium, scarring from excimer laser surgery, scarring from glaucoma filtering surgery, macular degeneration, crest syndromes, solid neoplasms, vascular tumours, melanoma and Kaposi's sarcoma. The present amino acid sequence represents a human cell surface protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell-surface protesse-associated disease; cancer; ocular disease; cardiovascular disease; chronic inflammatory disease; wound; circulatory diseate; chronic inflammatory disease; wound; circulatory diseater; dermatological disorder; retenuatorial arthritis; psoriasis; diabetic retinopathy; pterygium; excimer laser surgery scarring; glaucoma filtering surgery scarring; macular degeneration; crest syndrome; solid neoplasm; vascular tumour; melanoma; Kaposi's sarcoma; human; cell surface protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel conjugate useful for treating cell-surface protease-associated disease, comprises a therapeutic agent and a peptidic or nucleic acis substrate linked to it optionally by a peptidic linker.
                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
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                                                                             SAAHCYIDDRGFRYSDFTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
                                                                                                                                                                                                                                                                                         SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                                                          GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPYYPGHYPPNIDCTWNIEVPNNQHVKVSFKFFYLLEPGVPAGTCPKDYVEINGEKYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPYYPGHYPENIDCTWNIEVPNNQHVKVRFKFFYLLEPRRACGTCPKDYVEINGEKYCGE
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  ALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVIN
                                                                                                                                                   CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV
                                                                                                                                                                                                                                                         SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED
                                                                                                                                                                                                                                                                                                                                                            GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCD
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                                                SAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDI
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99.3%; Pred. No. 1.2¢
tive 0; Mismatches
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                                                                                                             Query Match
Best Local
Matches 67
                                                                                                                                                                                                                                                                                                       The present sequence is the protein sequence of human MTSP1 (matriptase), a serine protease that is expressed in epithelial cancer and normal tissue. In an example from the invention, the protein sequence of the protease domain of MTSP1 was used to search a human genome database. A protease was identified and designated serine protease 16 or CVSP16. CVSP16 CDNA ADI28863 was subsequently cloned from a human liver CDNA library by PCR. CVSP16 polypeptides exhibit protease activity as a single chain or as a multi-chain form. Methods are provided for identifying compounds that modulate the protease activity. CVSP16 polypeptides also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease 16 polypeptides, useful for diagnosing, preventing treating cancer (e.g. breast cancer) or for identifying compounds that may be used for modulating the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002; 2002US-0394347P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-2003; 2003WO-US020959
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                                                                                                                                                                                                                             Sequence 855 AA;
                                                                                                                                                                                                                                                                                  serve as tumour markers.
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; serine protease.
                                                                                                                                          Similarity
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  MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG
                                   MAEERVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205pp; English.
                                                                                                          Score 3754; DB 8;
Pred. No. 1.2e-240;
0; Mismatches 5;
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                                                                                                                                                                                                                                                           Human; transmembrane serine protease; MTSP; cell surface protease; plasmin; prostate specific antigen; PSA; proliferative disease; cell-surface protease-associated disease; autoimmune disease; inflammatory disease-associated disease; endoorine disease; cancer; ocular disorder; cardiovascular disorder; chronic inflammatory disease; wound; circulatory disorder; dermatological disorder; restenosis; rheumatoid arthritis; psoriasis; diabetic retinopathy; laser surgery scarring; glaucoma filtering surgery scarring; viral disease; macular degeneration; CREST syndrome; bacterial infection; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-2004
                                                                                                                                                                                                       solid neoplasm; vascular tumour; lung; colon; prostate; melanoma;
Kaposi's sarcoma; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transmembrane serine protease (MTSP) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ46895 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC optionally through a linker or peptidic linker, where the peptidic CC substrate is proteolytically cleaved by a cell surface protease or a CC soluble, released or shed form conjugate to liberate the agent and the CC conjugate is not substantially cleaved by plasmin or prostate specific CC involves administering a conjugate to a subject, where the disease is CC preferably a proliferative diseases or a cell-surface protease-associated CC disease. The diseases include autoimmune diseases, inflammatory diseases, CC infectious diseases and endocrine diseases. The conjugate is useful for treating a cell-surface protease-associated disease, which involves administering a conjugate comprising an agent and a peptidic substrate to CC a subject exhibiting symptoms of a cell-surface protease-associated CC as subject exhibiting symptoms of a cell-surface protease-associated CC as subject exhibiting symptoms of a cell-surface protease-associated CC cardiovascular disorders, chronic inflammatory diseases, wounds, CC cardiovascular disorders, dermatological disorders, restenosis, rheumatoid CC cardivitis, psoriasis, diabetic retinopathies, scarring from laser CC curgery, scarring from glaucoma filtering surgery, macular degeneration, CC CREST syndrome, bacterial infections, viral diseases, solid neoplasms and CC wascular tumours such as lung cancer, colon cancer, solid neoplasms and color protease (MTSP) polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 678; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conjugate useful for treating e.g. cancer, cell-surface passociated diseases, comprising a peptidic substrate or resubstrate linked to a therapeutic agent through a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 855 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a conjugate comprising a therapeutic agent and tidic substrate or nucleic acid substrate linked to the agent
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                                                                                                 GWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSVNDCGDNSDEQGCSCPAQTFRC
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23-DEC-1999; 99US-00471275 21-JAN-2000; 2000US-00488725 25-APR-2000; 2000US-00552317

22-DEC-2000; 2000WO-US035017

Claim 20;

Page 237; 1217pp; English

Isolated human polymucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

2001-457603/49.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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CC AAM25963. The proteins can have activities based on the tissues and cells CC they are expressed in, such as: antiinflammatory; antirheumatic; CC antiarthricic; immunosuppressive; antibacterial; endocrine; cardiant; CC cardiovascular; antianaemic; antiangergant; haemostatic; vulnerary; CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antiparkineonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine componists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, canaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, costeoporosis, severe combined immunodeficiency, eczema, allergic costeoporosis, stevene combined immunodeficiency, eczema, allergic combined immunodeficiency, eczema, allergic continitis, asthma, diabetes, cancer, multiple sclerosis, depression, alicerres disease, Parkinson's disease, neurodegenerative and Sequence 851 AA; neurological disorders

Query Match
Best Local Similarity
Matches 676; Conserv Conservative 98.8%; Score 3745; DB 4; Length 851; 99.0%; Pred. No. 4.6e-240; htive 1; Mismatches 6; Indels 0 0

589 421 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV 480 CSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLV

648

529

361

SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED 420

SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKED

588

199 RNKPGVYTRLPLFRDWIKENTGV 683

QTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQ

828

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769

밁 829 RNKPGVYTRLPLFRDWIKENTGV 851

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